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(21) International Application Number: PCT/JP99/06412 (22) International Filing Date: 17 November 1999 (17.11.99) (30) Priority Data: <table border="0"> <tr> <td>10/326255</td> <td>17 November 1998 (17.11.98)</td> <td>JP</td> </tr> <tr> <td>10/364315</td> <td>22 December 1998 (22.12.98)</td> <td>JP</td> </tr> <tr> <td>11/69811</td> <td>16 March 1999 (16.03.99)</td> <td>JP</td> </tr> <tr> <td>11/119299</td> <td>27 April 1999 (27.04.99)</td> <td>JP</td> </tr> <tr> <td>11/138169</td> <td>19 May 1999 (19.05.99)</td> <td>JP</td> </tr> </table> (71) Applicants (for all designated States except US): SAGAMI CHEMICAL RESEARCH CENTER [JP/JP]; 4-1, Nishi-Ohnuma 4-chome, Sagamihara-shi, Kanagawa 229-0012 (JP). PROTEGENE INC. [JP/JP]; 2-20-3, Naka-cho, Meguro-ku, Tokyo 153-0065 (JP). (72) Inventors; and (75) Inventors/Applicants (for US only): KATO, Seishi [JP/JP]; 3-46-50, Wakamatsu, Sagamihara-shi, Kanagawa 229-0014 (JP). KIMURA, Tomoko [JP/JP]; 302, 4-1-28, Nishiikuta, Tama-ku, Kawasaki-shi, Kanagawa 214-0037 (JP).		10/326255	17 November 1998 (17.11.98)	JP	10/364315	22 December 1998 (22.12.98)	JP	11/69811	16 March 1999 (16.03.99)	JP	11/119299	27 April 1999 (27.04.99)	JP	11/138169	19 May 1999 (19.05.99)	JP	(74) Agents: AOYAMA, Tamotsu et al.; Aoyama & Partners, IMP Building, 3-7, Shiromi 1-chome, Chuo-ku, Osaka-shi, Osaka 540-0001 (JP). (81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
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(54) Title: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAS ENCODING THESE PROTEINS (57) Abstract <p>The present invention provides human proteins having hydrophobic domains, DNAs encoding these proteins, and expression vectors for these DNAs as well as eukaryotic cells expressing these DNAs.</p>																	

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DESCRIPTION

Human Proteins Having Hydrophobic
Domains and DNAs Encoding These Proteins

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TECHNICAL FIELD

The present invention relates to human proteins having hydrophobic domains, DNAs encoding these proteins, and expression vectors for these DNAs as well as eukaryotic cells expressing these DNAs. The proteins of the present invention can be employed as pharmaceuticals or as antigens for preparing antibodies against these proteins. The human cDNAs of the present invention can be utilized as probes for genetic diagnosis and gene sources for gene therapy. Furthermore, the cDNAs can be utilized as gene sources for large-scale production of the proteins encoded by these cDNAs. Cells into which these genes are introduced to express secretory proteins or membrane proteins in large quantity can be utilized for detection of the corresponding receptors or ligands, screening of novel small molecule pharmaceuticals and the like.

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20BACKGROUND ART

Cells secrete many proteins extracellularly. These secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport, the biophylaxis, and the like of the cells. Unlike intracellular proteins, the secretory proteins exert their actions outside the cells. Therefore, they can be administered in the intracorporeal manner such as the injection or the drip, so that they possess hidden

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potentialities as pharmaceuticals. In fact, a number of human secretory proteins such as interferons, interleukins, erythropoietin, thrombolytic agents and the like have been currently employed as pharmaceuticals. In addition, 5 secretory proteins other than those described above are undergoing clinical trials for developing their use as pharmaceuticals. It is believed that the human cells produce many unknown secretory proteins. Availability of these secretory proteins as well as genes encoding them is 10 expected to lead to development of novel pharmaceuticals utilizing these proteins.

On the other hand, membrane proteins play important roles, as signal receptors, ion channels, transporters and the like in the material transport and the signal 15 transduction through the cell membrane. Examples thereof include receptors for various cytokines, ion channels for the sodium ion, the potassium ion, the chloride ion and the like, transporters for saccharides and amino acids and the like. The genes for many of them have already been cloned. 20 It has been clarified that abnormalities of these membrane proteins are involved in a number of previously cryptogenic diseases. Therefore, discovery of a new membrane protein is expected to lead to elucidation of the causes of many diseases, so that isolation of new genes encoding the 25 membrane proteins has been desired.

Heretofore, due to difficulty in the purification from human cells, many of these secretory proteins and membrane proteins have been isolated by genetic approaches. A general method is the so-called expression cloning method, in which 30 a cDNA library is introduced into eukaryotic cells to express cDNAs, and the cells secreting, or expressing on the surface of membrane, the protein having the activity of

interest are then screened. However, only genes for proteins with known functions can be cloned by using this method.

In general, a secretory protein or a membrane protein possesses at least one hydrophobic domain within the protein.
5 After synthesis in the ribosome, such domain works as a secretory signal or remains in the phospholipid membrane to be entrapped in the membrane. Accordingly, if the existence of a highly hydrophobic domain is observed in the amino acid sequence of a protein encoded by a cDNA when the whole base
10 sequence of the full-length cDNA is determined, it is considered that the cDNA encodes a secretory protein or a membrane protein.

OBJECTS OF THE INVENTION

15 The main object of the present invention is to provide novel human proteins having hydrophobic domains, DNAs encoding these proteins, and expression vectors for these DNAs as well as transformed eukaryotic cells that are capable of expressing these DNAs. This object as well as
20 other objects and advantages of the present invention will become apparent to those skilled in the art from the following description with reference to the accompanying drawings.

BRIEF DESCRIPTION OF DRAWINGS

Fig. 1 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02539.

Fig. 2 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02770.

30 Fig. 3 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02869.

Fig. 4 illustrates the hydrophobicity/hydrophilicity

profile of the protein encoded by clone HP02956.

Fig. 5 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02962.

Fig. 6 illustrates the hydrophobicity/hydrophilicity
5 profile of the protein encoded by clone HP03014.

Fig. 7 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10608.

Fig. 8 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10609.

10 Fig. 9 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10611.

Fig. 10 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10617.

Fig. 11 illustrates the hydrophobicity/hydrophilicity
15 profile of the protein encoded by clone HP02837.

Fig. 12 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02991.

Fig. 13 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03063.

20 Fig. 14 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03091.

Fig. 15 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03092.

Fig. 16 illustrates the hydrophobicity/hydrophilicity
25 profile of the protein encoded by clone HP03116.

Fig. 17 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10618.

Fig. 18 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10619.

30 Fig. 19 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10622.

Fig. 20 illustrates the hydrophobicity/hydrophilicity

profile of the protein encoded by clone HP10625.

Fig. 21 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02883.

Fig. 22 illustrates the hydrophobicity/hydrophilicity
5 profile of the protein encoded by clone HP03140.

Fig. 23 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10628.

Fig. 24 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10629.

10 Fig. 25 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10635.

Fig. 26 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10636.

Fig. 27 illustrates the hydrophobicity/hydrophilicity
15 profile of the protein encoded by clone HP10640.

Fig. 28 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10644.

Fig. 29 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10656.

20 Fig. 30 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10672.

Fig. 31 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03194.

Fig. 32 illustrates the hydrophobicity/hydrophilicity
25 profile of the protein encoded by clone HP03219.

Fig. 33 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03236.

Fig. 34 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03237.

30 Fig. 35 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03267.

Fig. 36 illustrates the hydrophobicity/hydrophilicity

profile of the protein encoded by clone HP03270.

Fig. 37 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03298.

Fig. 38 illustrates the hydrophobicity/hydrophilicity
5 profile of the protein encoded by clone HP10631.

Fig. 39 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10658.

Fig. 40 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10663.

10 Fig. 41 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03165.

Fig. 42 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03266.

Fig. 43 illustrates the hydrophobicity/hydrophilicity
15 profile of the protein encoded by clone HP03287.

Fig. 44 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10665.

Fig. 45 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10669.

20 Fig. 46 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10670.

Fig. 47 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10671.

Fig. 48 illustrates the hydrophobicity/hydrophilicity
25 profile of the protein encoded by clone HP10673.

Fig. 49 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10675.

Fig. 50 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10683.

SUMMARY OF THE INVENTION

As the result of intensive studies, the present inventors have successfully cloned cDNAs encoding proteins having hydrophobic domains from the human full-length cDNA bank, thereby completing the present invention. Thus, the present invention provides a human protein having hydrophobic domain(s), namely a protein comprising any one of an amino acid sequence selected from the group consisting of SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130. Moreover, the present invention provides a DNA encoding the above-mentioned protein, exemplified by a cDNA comprising any one of a base sequence selected from the group consisting of SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131 to 150 as well as an expression vector that is capable of expressing such DNA by in vitro translation or in eukaryotic cells and a transformed eukaryotic cell that is capable of expressing such DNA and of producing the above-mentioned protein.

DETAILED DESCRIPTION OF THE INVENTION

The proteins of the present invention can be obtained, for example, by a method for isolating proteins from human organs, cell lines or the like, a method for preparing peptides by the chemical synthesis based on the amino acid sequence of the present invention, or a method for producing proteins by the recombinant DNA technology using the DNAs encoding the hydrophobic domains of the present invention. Among these, the method for producing proteins by the recombinant DNA technology is preferably employed. For example, the proteins can be expressed in vitro by preparing an RNA by in vitro transcription from a vector having the

cdNA of the present invention, and then carrying out in vitro translation using this RNA as a template. Alternatively, introduction of the translated region into a suitable expression vector by the method known in the art may lead to expression of a large amount of the encoded protein in prokaryotic cells such as *Escherichia coli*, *Bacillus subtilis*, etc., and eukaryotic cells such as yeasts, insect cells, mammalian cells, etc.

In the case where the protein of the present invention is produced by expressing the DNA by in vitro translation, the protein of the present invention can be produced in vitro by introducing the translated region of this cdNA into a vector having an RNA polymerase promoter, and then adding the vector to an in vitro translation system such as a rabbit reticulocyte lysate or a wheat germ extract, which contains an RNA polymerase corresponding to the promoter. The RNA polymerase promoters are exemplified by T7, T3, SP6 and the like. The vectors containing these RNA polymerase promoters are exemplified by pKA1, pCDM8, pT3/T7 18, pT7/3 19, pBluescript II and the like. Furthermore, the protein of the present invention can be expressed in the secreted form or the form incorporated in the microsome membrane when a canine pancreas microsome or the like is added to the reaction system.

In the case where the protein of the present invention is produced by expressing the DNA in a microorganism such as *Escherichia coli* etc., a recombinant expression vector in which the translated region of the cdNA of the present invention is introduced into an expression vector having an origin which is capable of replicating in the microorganism, a promoter, a ribosome-binding site, a cdNA-cloning site, a terminator and the like is constructed. After transformation

of the host cells with this expression vector, the resulting transformant is grown, whereby the protein encoded by the cDNA can be produced in large quantity in the microorganism. In this case, a protein fragment containing any translated region can be obtained by adding an initiation codon and a termination codon in front of and behind the selected translated region to express the protein. Alternatively, the protein can be expressed as a fusion protein with another protein. Only the portion of the protein encoded by the cDNA can be obtained by cleaving this fusion protein with a suitable protease. The expression vectors for *Escherichia coli* are exemplified by the pUC series, pBluescript II, the pET expression system, the pGEX expression system and the like.

15 In the case where the protein of the present invention is produced by expressing the DNA in eukaryotic cells, the protein of the present invention can be produced as a secretory protein, or as a membrane protein on the cell-membrane surface, by introducing the translated region of the cDNA into an expression vector for eukaryotic cells that has a promoter, a splicing region, a poly(A) addition site and the like, and then introducing the vector into the eukaryotic cells. The expression vectors are exemplified by pKA1, pED6dpc2, pCDM8, pSVK3, pMSG, pSVL, pBK-CMV, pBK-RSV, EBV vectors, pRS, pYES2 and the like. Examples of eukaryotic cells to be used in general include mammalian cultured cells such as monkey kidney COS7 cells, Chinese hamster ovary CHO cells and the like, budding yeasts, fission yeasts, silkworm cells, *Xenopus* oocytes and the like. Any eukaryotic cells may be used as long as they are capable of expressing the proteins of the present invention. The expression vector can be introduced into the eukaryotic cells by using a method

known in the art such as the electroporation method, the calcium phosphate method, the liposome method, the DEAE-dextran method and the like.

After the protein of the present invention is expressed
5 in prokaryotic cells or eukaryotic cells, the protein of interest can be isolated from the culture and purified by a combination of separation procedures known in the art. Examples of the separation procedures include treatment with a denaturing agent such as urea or a detergent, sonication,
10 enzymatic digestion, salting-out or solvent precipitation, dialysis, centrifugation, ultrafiltration, gel filtration, SDS-PAGE, isoelectric focusing, ion-exchange chromatography, hydrophobic chromatography, affinity chromatography, reverse phase chromatography and the like.

15 The proteins of the present invention also include peptide fragments (of 5 amino acid residues or more) containing any partial amino acid sequences in the amino acid sequences represented by SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130. These peptide fragments
20 can be utilized as antigens for preparation of antibodies. Among the proteins of the present invention, those having the signal sequences are secreted in the form of mature proteins after the signal sequences are removed. Therefore, these mature proteins shall come within the scope of the
25 protein of the present invention. The N-terminal amino acid sequences of the mature proteins can be easily determined by using the method for the determination of cleavage site of a signal sequence [JP 8-187100 A]. Furthermore, some membrane proteins undergo the processing on the cell surface to be
30 converted to the secreted forms. Such proteins or peptides in the secreted forms shall also com within the scope of the protein of the present invention. In the case where

sugar chain-binding sites are present in the amino acid sequences of the proteins, expression of the proteins in appropriate eukaryotic cells affords the proteins to which sugar chains are attached. Accordingly, such proteins or peptides to which sugar chains are attached shall also come within the scope of the protein of the present invention.

The DNAs of the present invention include all the DNAs encoding the above-mentioned proteins. These DNAs can be obtained by using a method for chemical synthesis, a method for cDNA cloning and the like.

The cDNAs of the present invention can be cloned, for example, from cDNA libraries derived from the human cells. The cDNAs are synthesized by using poly(A)⁺ RNAs extracted from human cells as templates. The human cells may be cells delivered from the human body, for example, by the operation or may be the cultured cells. The cDNAs can be synthesized by using any method such as the Okayama-Berg method [Okayama, H. and Berg, P., Mol. Cell. Biol. 2: 161-170 (1982)], the Gubler-Hoffman method [Gubler, U. and Hoffman, J., Gene 25: 263-269 (1983)] and the like. However, it is desirable to use the capping method [Kato, S. et al., Gene 150: 243-250 (1994)], as exemplified in Examples, in order to obtain a full-length clone in an effective manner. In addition, commercially available human cDNA libraries can be utilized.

The cDNAs of the present invention can be cloned from the cDNA libraries by synthesizing an oligonucleotide on the basis of base sequences of any portion in the cDNA of the present invention and screening the cDNA libraries using this oligonucleotide as a probe for colony or plaque hybridization according to a method known in the art. In addition, the cDNA fragments of the present invention can be prepared from an mRNA isolated from human cells by the RT-

PCR method in which oligonucleotides which hybridize with both termini of the cDNA fragment of interest are synthesized, which are then used as the primers.

5 The cDNAs of the present invention are characterized in that they comprise any one of the base sequences represented by SEQ ID NOS: 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140 or the base sequences represented by SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120, and 141 to 150. Table 1 summarizes the clone number (HP number), the cells
10 from which the cDNA clone was obtained, the total base number of the cDNA, and the number of the amino acid residues of the encoded protein, for each of the cDNAs.

Table 1

SEQ ID NO	HP number	Cells	Base number	Number of amino acid residues
1, 11, 21	HP02539	Saos-2	4485	647
2, 12, 22	HP02770	HT-1080	1509	350
3, 13, 23	HP02869	KB	3059	206
4, 14, 24	HP02956	KB	2367	213
5, 15, 25	HP02962	KB	2355	595
6, 16, 26	HP03014	Liver	1024	264
7, 17, 27	HP10608	Saos-2	1237	343
8, 18, 28	HP10609	KB	1332	244
9, 19, 29	HP10611	KB	1932	303
10, 20, 30	HP10617	HT-1080	1124	160
31, 41, 51	HP02837	HT-1080	4473	1445
32, 42, 52	HP02991	KB	2630	582
33, 43, 53	HP03063	HT-1080	1472	410
34, 44, 54	HP03091	Liver	1652	483
35, 45, 55	HP03092	Liver	2112	607
36, 46, 56	HP03116	KB	1087	314
37, 47, 57	HP10618	HT-1080	1694	94
38, 48, 58	HP10619	HT-1080	1522	218
39, 49, 59	HP10622	Liver	1591	460
40, 50, 60	HP10625	Liver	1249	216
61, 71, 81	HP02883	KB	4027	392
62, 72, 82	HP03140	HT-1080	2495	497
63, 73, 83	HP10628	HT-1080	1617	417
64, 74, 84	HP10629	WERI-RB	3269	649
65, 75, 85	HP10635	WERI-RB	458	93
66, 76, 86	HP10636	HT-1080	1712	425
67, 77, 87	HP10640	WERI-RB	1055	149
68, 78, 88	HP10644	WERI-RB	1616	396
69, 79, 89	HP10656	PMA-U937	1860	350
70, 80, 90	HP10672	Thymus	783	153
91, 101, 111	HP03194	KB	3438	303

92, 102, 112	HP03219	PMA-U937	1144	283
93, 103, 113	HP03236	HT-1080	2339	488
94, 104, 114	HP03237	HT-1080	1765	182
95, 105, 115	HP03267	Liver	1418	184
96, 106, 116	HP03270	PMA-U937	1211	140
97, 107, 117	HP03298	PMA-U937	1099	153
98, 108, 118	HP10631	WERI-RB	3489	173
99, 109, 119	HP10658	HT-1080	931	75
100, 110, 120	HP10663	PMA-U937	1123	159
121, 131, 141	HP03165	KB	3234	636
122, 132, 142	HP03266	HT-1080	2490	318
123, 133, 143	HP03287	Thymus	1465	82
124, 134, 144	HP10665	HT-1080	917	247
125, 135, 145	HP10669	WERI-RB	1306	206
126, 136, 146	HP10670	WERI-RB	2022	432
127, 137, 147	HP10671	Thymus	1227	306
128, 138, 148	HP10673	Thymus	2210	555
129, 139, 149	HP10675	Thymus	1493	250
130, 140, 150	HP10683	PMA-U937	1264	174

The same clones as the cDNAs of the present invention can be easily obtained by screening the cDNA libraries constructed from the human cell lines or human tissues utilized in the present invention using an oligonucleotide probe synthesized on the basis of the base sequence of the cDNA provided in any one of SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120, and 131 to 150.

In general, the polymorphism due to the individual differences is frequently observed in human genes. Accordingly, any cDNA in which one or plural nucleotides are added, deleted and/or substituted with other nucleotides in SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120, and 131 to 150 shall come within the scope of the present

invention.

Similarly, any protein in which one or plural amino acids are added, deleted and/or substituted with other amino acids resulting from the above-mentioned changes shall come
5 within the scope of the present invention, as long as the protein possesses the activity of the protein having any one of the amino acid sequences represented by SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130.

The cDNAs of the present invention also include cDNA
10 fragments (of 10 bp or more) containing any partial base sequence in the base sequences represented by SEQ ID NOS: 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140 or in the base sequences represented by SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120, and 141 to 150. Also, DNA
15 fragments consisting of a sense strand and an anti-sense strand shall come within this scope. These DNA fragments can be utilized as the probes for the genetic diagnosis.

In addition to the activities and uses described above, the polynucleotides and proteins of the present invention
20 may exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of
25 polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention
30 can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use;

as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern
5 gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source
10 of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of
15 expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example,
20 in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors
25 of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit
30 another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological

fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to
5 isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction.
10 Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for
15 commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory
20 Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

25 Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases
30 the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the

form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

5 Cytokine and Cell Proliferation/Differentiation
 Activity

 A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or
10 may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of
15 cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165,
20 HT2, CTLL2, TF-1, Mo7e and CMK.

 The activity of a protein of the invention may, among other means, be measured by the following methods:

 Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in
25 Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol.
30 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol.

149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ , Schreiber, R.D. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without
5 limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines
10 and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

15 Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment
20 of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune
25 deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the
30 present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as

candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

5 Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune
10 thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly
15 allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

 Using the proteins of the invention it may also be
20 possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by
25 suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing
30 non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent

has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen
5 functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For
10 example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the
15 transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an
20 activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function
25 in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte
30 antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a

subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating

autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the

transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

5 In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can
10 be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the
15 expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell.
20 Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary
25 costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected
30 with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β , microglobulin protein or an MHC class

II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J.

Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses
5 and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In
10 vitro antibody production, Mond, J.J. and Brunswick, M. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly
15 Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse
20 Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify,
25 among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine
30 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994;

Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

5 Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 10 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 15 1:639-648, 1992.

 Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et 20 al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

 A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the 25 treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells 30 alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to

stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) 5 useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as 10 thrombocytopenia, and generally for use in place of or complementary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic 15 utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or 20 ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among 25 other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence 30 embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and

Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is

not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as
5 open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

10 A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming
15 cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by
20 inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or
25 other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing
30 protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and

in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head

trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

5 Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds and the like.

10 It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including
15 vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

20 A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful
25 for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

30 Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon);

International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without
5 limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

10 A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of
15 follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals.
20 Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may be useful as a fertility inducing therapeutic, based upon the
25 ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime
30 reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among

other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; 5 Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic 10 or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a 15 desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or 20 neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or 25 indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing 30 such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among

other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke)).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include,

without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-
5 474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such
10 receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules
15 (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors
20 of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among
25 other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing
30 Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987;

Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

5 Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

20 Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly

(such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic

lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

10

Examples

The present invention is specifically illustrated in more detail by the following Examples, but Examples are not intended to restrict the present invention. The basic procedures with regard to the recombinant DNA and the enzymatic reactions were carried out according to the literature ["Molecular Cloning. A Laboratory Manual", Cold Spring Harbor Laboratory, 1989]. Unless otherwise stated, restriction enzymes and various modifying enzymes to be used were those available from Takara Shuzo. The buffer compositions and the reaction conditions for each of the enzyme reactions were as described in the attached instructions. The cDNA synthesis was carried out according to the literature [Kato, S. et al., Gene 150: 243-250 (1994)].

(1) Selection of cDNAs Encoding Proteins Having Hydrophobic Domains

The cDNA library of fibrosarcoma cell line HT-1080 (WO 98/11217), the cDNA library of osteosarcoma cell line Saos-2 (WO 97/33993), the cDNA library of epidermoid carcinoma cell line KB (WO 98/11217) and the cDNA library of liver tissue delivered by the operation (WO 98/21328) were used as the

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cdna libraries. Additionally, the cdna libraries constructed from phorbol ester-stimulated histiocytic lymphoma cell line U937 (ATCC CRL 1593) mRNA, human retinoblastoma cell line WERI-RB (ATCC HTB 169) mRNA and human thymus mRNA (Clontech) were also used. Full-length cdna clones were selected from the respective libraries and the whole base sequences thereof were determined to construct a homo-protein cdna bank consisting of the full-length cdna clones. The hydrophobicity/hydrophilicity profiles were determined for the proteins encoded by the full-length cdna clones registered in the homo-protein cdna bank by the Kyte-Doolittle method [Kyte, J. & Doolittle, R. F., J. Mol. Biol. 157: 105-132 (1982)] to examine the presence or absence of a hydrophobic region. A clone that has a hydrophobic region being assumed as a secretory signal or a transmembrane domain in the amino acid sequence of the encoded protein was selected as a clone candidate.

(2) Protein Synthesis by In Vitro Translation

The plasmid vector bearing the cdna of the present invention was used for in vitro transcription/translation with a T_NT rabbit reticulocyte lysate kit (Promega). In this case, [³⁵S]methionine was added to label the expression product with a radioisotope. Each of the reactions was carried out according to the protocols attached to the kit. Two micrograms of the plasmid was subjected to the reaction at 30°C for 90 minutes in the reaction solution of a total volume of 25 µl containing 12.5 µl µ of T_NT rabbit reticulocyte lysate, 0.5 µl of a buffer solution (attached to the kit), 2 µl of an amino acid mixture (without methionine), 2 µl of [³⁵S]methionine (Amersham) (0.37 MBq/µl), 0.5 µl of T7 RNA polymerase, and 20 U of RNasin. The experiment in the presence of a membrane system was carried

out by adding 2.5 μ l of a canine pancreas microsome fraction (Promega) to the reaction system. To 3 μ l of the reaction solution was added 2 μ l of the SDS sampling buffer (125 mM Tris-hydrochloride buffer, pH 6.8, 120 mM 2-mercaptoethanol, 2% SDS solution, 0.025% bromophenol blue and 20% glycerol) and the resulting mixture was heated at 95°C for 3 minutes and then subjected to SDS-polyacrylamide gel electrophoresis. The molecular weight of the translation product was determined by carrying out the autoradiography.

10 (3) Expression in COS7

Escherichia coli cells harboring the expression vector for the protein of the present invention were cultured at 37°C for 2 hours in 2 ml of the 2xYT culture medium containing 100 μ g/ml of ampicillin, the helper phage M13K07 (50 μ l) was added, and the cells were then cultured at 37°C overnight. Single-stranded phage particles were obtained by polyethylene glycol precipitation from a supernatant separated by centrifugation. The particles were suspended in 100 μ l of 1 mM Tris-0.1 mM EDTA, pH 8 (TE).

20 The cultured cells derived from monkey kidney, COS7, were cultured at 37°C in the presence of 5% CO₂ in the Dulbecco's modified Eagle's medium (DMEM) containing 10% fetal calf serum. 1 x 10⁵ COS7 cells were inoculated into a 6-well plate (Nunc, well diameter: 3 cm) and cultured at 25 37°C for 22 hours in the presence of 5% CO₂. After the medium was removed, the cell surface was washed with a phosphate buffer solution followed by DMEM containing 50 mM Tris-hydrochloride (pH 7.5) (TDMEM). A suspension containing 1 μ l of the single-stranded phage suspension, 0.6 ml of the 30 DMEM medium and 3 μ l of TRANSFECTAMTM (IBF) was added to the cells and the cells were cultured at 37°C for 3 hours in the presence of 5% CO₂. After the sample solution was removed,

the cell surface was washed with TDMEM, 2 ml per well of DMEM containing 10% fetal calf serum was added, and the cells were cultured at 37°C for 2 days in the presence of 5% CO₂. After the medium was exchanged for a medium containing
5 [35S]cystine or [35S]methionine, the cells were cultured for one hour. After the medium and the cells were separated each other by centrifugation, proteins in the medium fraction and the cell membrane fraction were subjected to SDS-PAGE.

(4) Clone Examples

10 <HP02539> (SEQ ID NOS: 1, 11, and 21)

Determination of the whole base sequence of the cDNA insert of clone HP02539 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 188-bp 5'-untranslated region, a 1944-bp ORF,
15 and a 2353-bp 3'-untranslated region. The ORF encodes a protein consisting of 647 amino acid residues and there existed a putative secretory signal at the N-terminus and six putative transmembrane domains at the C-terminus. Figure 1 depicts the hydrophobicity/hydrophilicity profile,
20 obtained by the Kyte-Doolittle method, of the present protein.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the mouse frizzled-1 (GenBank
25 Accession No. AF054623). Table 2 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the mouse frizzled-1 (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the
30 present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 90.4% in the entire

region.

Table 2

	HP	MAEEEAPKKSRAAGGGASWELCAGALSARLTEEGSGDAGRRRPPVDPRRLARQLLLLLLW
		****.***.***** * * ****.***.* * * .*.*****.***** *. *****
5	MM	MAEEAAPSESRAA--GRLSLELCAEALPGRREEVGHEDTASHRRPRADPRRWASGLLLLLLW
	HP	LLEAPLLLGVRAQAAGQGPGQGPQPPPPQQQSGQQYNGERGISVPDHGYCQPIS
		***** ** .*****.*****.*****.*****.*****
	MM	LLEAPLLLGVRAQAA----GQVSGPGQAPPPQPPQSGQQYNGERGISIPDHGYCQPIS
	HP	IPLCTDIAYNQTIMPNNLLGHTNQEDAGLEVHQFYPLVKVQCSAELKFFLCSMYAPVCTVL
10		*****.*****.*****.*****.*****.*****.*****.*****.*****
	MM	IPLCTDMAYNQTIMPNNLLGHTNQEDAGLEVHQFYPLVKVQCSAELKFFLCSMYAPVCTVL
	HP	EQALPPCRSLCERARQGCEALMNKFGFQWPDTLKCEKFPVHGAGELCVGQNTSDKGTPTP
		*****.*****.*****.*****.*****.*****.*****.*****.*****
	MM	EQALPPCRSLCERARQGCEALMNKFGFQWPDTLKCEKFPVHGAGELCVGQNTSDKGTPTP
15	HP	SLLPEFWTSNPQHGGGGHRRGGFPGGAGASERGFSCPRALKVPSYLNHFLGEKDCGAPC
		*****.*****.***.*****.*****.*****.*****.*****.*****
	MM	SLLPEFWTSNGQHGGGGYRGGYPGGAGTVERGKFSCPRALRVPSYLNHFLGEKDCGAPC
	HP	EPTKVYGLMYFGPEELRFSRTWIGIWSVLCCASTLFTVLTYLVDMPRFYSYPERPIIFLSG
		*****.*****.*****.*****.*****.*****.*****.*****.***
20	MM	EPTKVYGLMYFGPEELRFSRTWIGIWSVLCCASTLFTVLTYLVDMPRFYSYPERPIISLSG
	HP	CYTAVAVAYIAGFLEDRVVCNDKFAEDGARTVAQGTKKEGCTILEMMLYFFSMASSIWW
		*****.*****.*****.*****.*****.*****.*****.*****.*****
	MM	CYTAVAVAYIAGFLEDRVVCNDKFAEDGARTVAQGTNKEGCTILEMMLYFFSMASSIWW
	HP	VILSLTWFLAAGMKWGHEAIEANSQYFHAAWAVPAIKTITILALGQVDGDLVSGVCFVG
25		*****.*****.*****.*****.*****.*****.*****.*****.*
	MM	VILSLTWFLAAGMKWGHEAIEANSQYFHAAWAVPAIKTITILALGQVDGDLVSGVCFVG
	HP	LNNVDALRGFVLAPLFVYLFIGTSFLLAGFVSLFRIRTIMKHDGKTTEKLEKLMVRIGVF
		*****.*****.*****.*****.*****.*****.*****.*****.*****
	MM	LNNVDALRGFVLAPLFVYLFIGTSFLLAGFVSLFRIRTIMKHDGKTTEKLEKLMVRIGVF
30	HP	SVLYTVPATIVIACYFYEQAFRDQWERSWAQSCSYAIPCPHLQAGGGAPPHPPMSPDF
		*****.***.*****.*****.*****.*****.*****.*****.*****
	MM	SVLYTVPATIVIACYFYEQAFRDQWERSWAQSCSYAIPCPHLQAGGGVPPHPPMSPDF
	HP	TVFMIKYLMTLIVGITSGFVIWSGKTLNSWRKFYTRLTNSKQGETTV
		*****.*****.*****.*****.*****.*****.*****.*****.*****
35	MM	TVFMIKYLMTLIVGITSGFVIWSGKTLNSWRKFYTRLTNSKQGETTV

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA010020) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

10

<HP02770> (SEQ ID NOS: 2, 12, and 22)

Determination of the whole base sequence of the cDNA insert of clone HP02770 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 252-bp 5'-untranslated region, a 1053-bp ORF, and a 204-bp 3'-untranslated region. The ORF encodes a protein consisting of 350 amino acid residues and there existed two putative transmembrane domains. Figure 2 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 42 kDa that was somewhat larger than the molecular weight of 38,274 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human RING zinc finger protein (GenBank Accession No. AF037204). Table 3 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human RING zinc finger protein (ZN). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue

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similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 56.0% in the entire region.

5 Table 3

```

HP          MHPAAFPLPVVVAVLWGAAPTRGLIRATSDHNASMDFADLPALFGATLS
                                     .*** .*.***** ** *.
10 ZN MLLSIGMLMLSATQVYTILTVQLFAFLNLLPVEADILAYNFENASQTFDDLPARFGYRLP
HP QEGLQGFLVEAHPDNACSPIAPPPAPVNGSVFIALLRRFDCNFDLKVNAQKAGYGAAV
   .***.***.....*.***.***.***      .....*.***.*****.*****.*** **.
ZN AEGLKGFLINSKPENACEPIVPPPVKDNSSGTFIVLIRRLDCNFDIKVLNAQRAGYKAAI
HP VHNVNSNELLNMVWNSEEIQQQIWIPSVFIGERSSEYLRALFVYEKGARVLLVPDNTFPL
   ****.*...*. *.*. .* *****.*.. *.. *.*****.....***. ...**
15 ZN VHNVDSDDLISMGSN DIEVLKKIDIPSVFIGESSANSLKDEFTYEKGHLLVPEFSLPL
HP GYYLIPFTGIVGLLVLAMGAVMIARCIQHRKRLQRNRLTKEQLKQIPTHDYQKGDQYDVC
   .*****  ***. .. .  **.. .*.*. * .***** *.***.***.***.***.***
ZN EYYLIPFLIIVGICLILIVIFMITKQVDRHRARRNRLRKDQLKKLPVHKFKKGDEYDVC
HP AICLDEYEDGDKLRVLPCAHAHYSRCVDPWLTQTRKTCPICKQPVHRGPGDED-QEETQ
   *****.***.***.*****.*.*****.*** * ...**.* .....*
20 ZN AICLDEYEDGDKLRILPCSHAYHCKCVDPWLTKTTKTCPVCKQKVVP SQGSDSDTDSSQ
HP GQEEGDEGEPRDHPASERTPLLGSSTLPTSFGSLAPAPLVFPGPSTDPLSPSPSPVIL
   ...* .*. * .*
ZN EENEVTEHTPLLRPLASVSAQSFGALSESRS HQNMTESSDY EEDDNEDTDSSDAENEINE
25 HP V
ZN HDVVVQLQPNGERDYNIANTV

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30 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA434312) among ESTs. However, since they are partial sequences, it can not be judged whether or

not they encode the same protein as the protein of the present invention.

<HP02869> (SEQ ID NOS: 3, 13, and 23)

5 Determination of the whole base sequence of the cDNA
insert of clone HP02869 obtained from cDNA library of human
epidermoid carcinoma cell line KB revealed the structure
consisting of a 229-bp 5'-untranslated region, a 621-bp ORF,
and a 2209-bp 3'-untranslated region. The ORF encodes a
10 protein consisting of 206 amino acid residues and there
existed two putative transmembrane domains. Figure 3 depicts
the hydrophobicity/hydrophilicity profile, obtained by the
Kyte-Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
15 of 22 kDa that was almost identical with the molecular
weight of 22,367 predicted from the ORF.

Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
20 example, Accession No. AA278247) among ESTs. However, since
they are partial sequences, it can not be judged whether or
not they encode the same protein as the protein of the
present invention.

25 <HP02956> (SEQ ID NOS: 4, 14, and 24)

Determination of the whole base sequence of the cDNA
insert of clone HP02956 obtained from cDNA library of human
epidermoid carcinoma cell line KB revealed the structure
consisting of a 68-bp 5'-untranslated region, a 642-bp ORF,
30 and a 1657-bp 3'-untranslated region. The ORF encodes a
protein consisting of 213 amino acid residues and there
existed three putative transmembrane domains. Figure 4

depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 22 kDa that was almost identical with the
5 molecular weight of 23,902 predicted from the ORF. When expressed in COS7 cells, an expression product of about 20 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the
10 protein was similar to the human tetraspan NET-4 (GenBank Accession No. AF065389). Table 4 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human tetraspan NET-4 (TS).
15 Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 58.8% in the C-terminal region of 119 amino acid residues.

Table 4

	HP	MHY
5	TS MSGKHYKGPEVSCCIKYFIFGFNVIFWFLGITFLGIGLWAWNEKGVLSNISSITDLGGFD HP YRYSNAKVSCWYKYLIFSINIIFWLAGVVFGLVGLWAWSEKGVLSDLTKVTRMHGIDPVV	
	TS PVWLFLVVGVMFILGFAGCIGALRENTFLLKFFSVFLGIIFLELTAGVLAFFVKDWIK HP LVLVGVVMTLGFAGCVGALRENICLLNFNQCCGAYGPEDWDLNVYFNCSGASYSREKC	
10	TS DQLYFFINNNIRAYRDDIDLQNLIDFTQEYWQCCGAFGADDWNLNIYFNCTDSNASRERC HP GVPFSCCVPDPAQKVNTQCGYDVRIQLKSKWDESIFTKGCIQALESWLPRNIYIVAGVF *****.***..*.*****.*. . . . *.*****..*..*.****.*	
15	TS GVPFSCCTKOPAEDVINTQCGYDARQKPEVDQQIVIYTKGCVPOFEKWLQDNLTIVAGIF HP IAISLLQIFGIFLARTLISDIEAVKAGHHF *.*.***** **..*.*****.*. TS IGIALLLQIFGICLAQNLVSDIEAVRASW	

20 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. T05279) among ESTs. However, since
they are partial sequences, it can not be judged whether or
25 not they encode the same protein as the protein of the
present invention.

<HP02962> (SEQ ID NOS: 5, 15, and 25)

30 Determination of the whole base sequence of the cDNA
insert of clone HP02962 obtained from cDNA library of human
epidermoid carcinoma cell line KB revealed the structure
consisting of a 19-bp 5'-untranslated region, a 1788-bp ORF,
and a 548-bp 3'-untranslated region. The ORF encodes a

protein consisting of 595 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 5 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 70 kDa that was somewhat larger than the molecular weight of 67,549 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 85 kDa to which sugar chains are presumably attached. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from alanine at position 23. In addition, there exist in the amino acid sequence of this protein four sites at which N-glycosylation may occur (Asn-Thr-Thr at position 75, Asn-Gln-Thr at position 153, Asn-Tyr-Thr at position 237 and Asn-Ser-Ser at position 360).

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human hypothetical protein KIAA0584 (GenBank Accession No. AB011156). Table 5 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human hypothetical protein KIAA0584 (KI). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 52.9% in the entire region.

Table 5

HP MRAARAAPLLQLLLLLGPWLEAAGVAESPL--PAVVLAILARNAEHSL
*.. ***** *...*.*****.*.*
5 KI LAWSLLLLSSALLREGCRARFVAERDSEDDGEEPVVFPESPLQSPOTVLVAVILARNAHNTL
HP PHYLGALERLDYPRARMALWCATDHNVDNTTEMLQEWLAAGVDDYAADVWRPEGEPRFYP
.*.***..***.* *****.....**.* * **** ** **
KI PHFLGCLERLDYPKSRMAIWAATDHNVDNTTEIFREWLKNVQRLYHYVEWRPMDEPESYP
HP DEEGPKHWTKERHQFLMELKQEALTFAR-NWGADYILFADTDNILTNNQTLRLIMGQGLP
10 ** *****..* .*.***** **.* ***** *...*** **.*.....
KI DEIGPKHWPTSRFAHVMKLRQAALRTAREKW-SDYILFIDVDNFLTNPQTLNLLIAENKT
HP VVAPMLDSQTYYSNFWCGITPQGYRRTAEYFPTKNRQRRGCFRVPVMVHSTFLASLRAEG
*****..* *****.*...*.***** *...***** **.*.
KI IVAPMLESRLGLYSNFWCGITPKGFYKRTPDYVQIREWKRTGCFVPMVHSTFLIDLKREA
15 HP ADQLAFYPPHPNYTWPFDDIIVFAYACQAAGVSVHVCNEHRYGYMNVVPKSHQGLEDERV
*...*****..***.*****.....**.***.*...*..
KI SDKLTFYPPHQDYTWTFDDIIVFAFSSRQAGIQMYLCNREHYGYLPIPLKPHQTLQEDIE
HP NFIHLILEALVDGPRMQASAHVTRPSKRPSKIGFDEVFVISLARRPDRRERMLASLWEME
....*...*.*...*...*.*.*.*****.*...* ** *...*** **.*.*
20 KI NLIHVQIEAMIDRPPMEPSQYVSVVPKYPDKMGFDEIFMINLKRKDRDRMLRTLYEQE
HP ISGRVVDADVGDWMLNSSAIRNLGVDLLPGYQDPYSGRTLTKGEVGCFLSHYSIWEEVVAR
...*.***** **.*.....*****.*****.*...*...*****.*...*..
KI IEVKIVEAVDGKALNTSQLKALNIEMLPGYRDPYSSRPLTRGEIGCFLSHYSVWKEVIDR
HP GLARVLVFEDDVRFESNFRGLERLMEDVEAEKLSWDLIYLGRKQVN-PEKETAVEGLPG
25 *...*...***** **.*.....*.*.*****.....* *...***
KI ELEKTLVIEDDVRFEHQFKKLMKMLDNIDQAQLDWELIYIGRKMVQKEPEKAVPNVAN
HP LVVAGYSYWTLAYALRLAGARKLLASQPLRRMLPVDEFLPIMFDQHPNEQYKAHFWPRDL
.*.***.*...*...*...*...*.....*****.*...*...*...*...*..
KI LVEADYSYWTLGAVISLEGAQKLVGANPFGKMLPVDEFLPVMYNKHPVAEYKEYYESRDL
30 HP VAFSAQPLLAAPTHYAGDAEWLSDTETSSPWDDDSGRLLISWGSQ--KTLRSPRLDLTGS
****.*...*...*****.*...*...*...*...*...*...*...*...*...*..
KI KAFSAEPLLIYPTHYTGQPGYLSDTETSTIWDNETV-ATDWDRTTHAWKSRKQSRIYSNAK
HP SGHSLQPQPRDEL
....*
35 KI NTEALPPPTSLDTPVPSRDEL

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA358896) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

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<HP03014> (SEQ ID NOS: 6, 16, and 26)

Determination of the whole base sequence of the cDNA insert of clone HP03014 obtained from cDNA library of human liver revealed the structure consisting of a 26-bp 5'-untranslated region, a 795-bp ORF, and a 203-bp 3'-untranslated region. The ORF encodes a protein consisting of 264 amino acid residues and there existed one putative transmembrane domain. Figure 6 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 31 kDa that was somewhat larger than the molecular weight of 28,471 predicted from the ORF.

15

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the mouse WW domain-binding protein 1 (GenBank Accession No. U40825). Table 6 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the mouse WW domain-binding protein 1 (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue

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HP
MVASAKMGRAGTMVAEALR
**
MM MARASSRNSSEEAWGSLQAPQQQQSPAASSLEGAIWRRAGTQTRALDTILYHPQQSHLLR
10 HP ELCPGVNNQPYLCESGHCCGETGCCTYYYELWWFWLLWTVLILFSCCAFRHRRAKLRLQ
*****.*****.*****.*****.*****.*****.*****.*****
MM ELCPGVNTQPYLCETGHCCGETGCCTYYYELWWFWLLWTVLILFSCCAFRHRRAKLRLQ
HP QQQRQREINLLAYHGACHGAGPFPTGSLDLRFLSTFKPPAYEDVVHRPGTPPPPYTVAP
*****.*****.*****.*****.*****.*****.*****.*****
15 MM QQQRQREINLLAYHGACHGAGPVPTGSLDLRLLSAFKPPAYEDVVHHPGTPPPPYTVGP
HP GRPLTASSEQTCCSSSSCPAHFEGTNVEGVSSHQSAPPHQEGEPGAGVTPASTPPSCRY
* * *.*** * ***.***.***.*****.*** ***** **.*. *****
MM GYPWTTSSSECTRCSSSESSCSAHLEGTNVEGVSSQQSALPHQEGEPRAGLSPVHIPPSCRY
HP RRLTGDSGIELCPCPASGEGEPVKEVRVSATLPDLEDYSPCALPPESVPQIFPMGLSSSE
20 *****.*.*****.*.***. *****.*****.*.***. *****
MM RRLTGDSGIELCPCPDSSEGEPLKEARASASQPDLEDHSPCALPPDSVSQVPPMGLASSC
HP GDIP
*
MM GTSHK
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Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W24575) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10608> (SEQ ID NOS: 7, 17, and 27)

Determination of the whole base sequence of the cDNA insert of clone HP10608 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 23-bp 5'-untranslated region, a 1032-bp ORF, and a 182-bp 3'-untranslated region. The ORF encodes a protein consisting of 343 amino acid residues and there existed five putative transmembrane domains. Figure 7 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 37 kDa that was somewhat smaller than the molecular weight of 40,584 predicted from the ORF. When expressed in COS7 cells, an expression product of about 36 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T35406) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10609> (SEQ ID NOS: 8, 18, and 28)

Determination of the whole base sequence of the cDNA insert of clone HP10609 obtained from cDNA library of the human epidermoid carcinoma cell line KB revealed the structure consisting of a 38-bp 5'-untranslated region, a 735-bp ORF, and a 559-bp 3'-untranslated region. The ORF encodes a protein consisting of 244 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 8 depicts the hydrophobicity/hydrophilicity

profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was almost identical with the molecular weight of 27,756 predicted from the ORF.

5 When expressed in COS7 cells, an expression product of about 26 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Mycobacterium tuberculosis hypothetical protein Rv1147 (GenBank Accession No. Z95584).

10 Table 7 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the Mycobacterium tuberculosis hypothetical protein Rv1147 (MT). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that

15 of the protein of the present invention, respectively. The both proteins shared a homology of 31.7% in the entire region.

Table 7

HP MDILVPLLQLLVLLLTLPPLHMLALLGCWQPLCKSYFPYIMAVLTPKSNRKMESKKRELFS

5 MT MTSGAAASASRVDHPLFARIWPVVAHEAEAIRAL

HP QIKGLTGASGKVALLELGCCTGANFQFYPPGC-RVTCCLDPNPHFEKFLTKSMAENRHLOY

. *.* **.* *.*.*.*.* . *. *.*.*.*. . *.. .

MT RRENLAGLSGRV--LEVGAGVGTNFAYYPVAVEQVIAMEPEPRLAA-KARIAAADAPVPI

HP ERFVVPAGEDMRQLADGSMDDVVVCTLVLCVQSPRKVLQEVRRVLRPGGVLFWEHVAEP

10 . . *.*.*.*.*.*.*.*.*.* . * **.*.*.*.*.* * . *****

MT -VVTDKTVEEFRD--TETFDVVCSLVLCVSDPGAVLAHLRSLRRGGELRYLEHVASA

HP YGSWAFMWQQVFEPWTKHIGDGCCLTRETWKOLENAQFSEIQMERQPPPLKW--LPVGP

*... . . * .. ** *.* * * * . . * ***.

MT -GARGRVQRFDATFWPRLAGNCHTHRHTERAILDAGFVVDDSSRREWAFFAWVPLPVSEL

15 HP IMGKAVK

..* .

MT ALGRAHRT

20 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. T60981) among ESTs. However, since
they are partial sequences, it can not be judged whether or
25 not they encode the same protein as the protein of the
present invention.

<HP10611> (SEQ ID NOS: 9, 19, and 29)

Determination of the whole base sequence of the cDNA
30 insert of clone HP10611 obtained from cDNA library of the
human epidermoid carcinoma cell line KB revealed the
structure consisting of a 37-bp 5'-untranslated region, a
912-bp ORF, and a 983-bp 3'-untranslated region. The ORF

encodes a protein consisting of 303 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 9 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 31 kDa that was somewhat smaller than the molecular weight of 33,856 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 36 kDa. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from leucine at position 34. When expressed in COS7 cells, an expression product of about 35 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the 218 amino acid residues at the C-terminus of the protein matched with the amino acid sequence of human glucosidase II (SWISS-PROT Accession No. Q06003). However, no similarity was observed at the N-terminal portion.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H14054) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10617> (SEQ ID NOS: 10, 20, and 30)

Determination of the whole base sequence of the cDNA insert of clone HP10617 obtained from cDNA library of the human fibrosarcoma cell line HT-1080 revealed the structure

consisting of a 72-bp 5'-untranslated region, a 483-bp ORF, and a 569-bp 3'-untranslated region. The ORF encodes a protein consisting of 160 amino acid residues and there existed four putative transmembrane domains. Figure 10 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight. When expressed in COS7 cells, an expression product of about 17 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H67672) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP02837> (SEQ ID NOS: 31, 41, and 51)

Determination of the whole base sequence of the cDNA insert of clone HP02837 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 44-bp 5'-untranslated region, a 4338-bp ORF, and a 91-bp 3'-untranslated region. The ORF encodes a protein consisting of 1445 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 11 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 150 kDa that was almost identical with the molecular weight of 161,657 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the

cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from valine at position 22. In addition, there exist in the amino acid sequence of this protein 18 sites at which N-glycosylation
5 may occur.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human α -2 macroglobulin (SWISS-PROT Accession No. P01023). Table 8 shows the comparison
10 between amino acid sequences of the human protein of the present invention (HP) and the human α -2 macroglobulin (MG). Therein, the marks of - and * represent a gap and an amino acid residue identical with that of the protein of the present invention, respectively. The both proteins shared a
15 homology of 29.5% in the entire region.

Table 8

	HP	MQGPPLL--TAAHLLCVCTAALA-VAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVT
		* * * * * * * * * *
5	MG	MGKKNLLHPSLVLLLLVLLPTDASVSGKPQYMLVP-SLLHTETTEKGCVLLSYLNETVT
	HP	VKAELLKTASN-LTVSVLEAE-GVFEGKSFKTLTLPSPPLNSADEIYELRVTGRQTODEIL
		* * * * * * * * * *
	MG	VSASLESVRGNRSLFTDLEAENDVLHCVAF---AVPKSSSNEEVMFLTQVQKPTQ---E
	HP	FSNSTRLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSNLIL--IKDPKS
10		* * * * * * * * * *
	MG	FKKRTTVMVKNEDSLVFVQTDKSIYKPGQTVKFRVSMDFHP-LNELIPLVYIQDPKG
	HP	NLIQQWLSQQSDLGVISKTFQLSSHPI LGDWSIQVQ-VNDQTYQSFQVSEYVLPKFEVT
		* * * * * * * * * *
	MG	NRIAQWQSFQLEGGKQFSFPLSSEPFQGSYKVVQKKSGGRTEHPFTVEEFVLPKFEVQ
15	HP	LQTPLYCSMNSKHLNGTITAKYTYGKPVKGDVT----LTFLPLSFWGKKKNITKTFKING
		* * * * * * * * * *
	MG	VTVPKIITILEEEMNVSVCGLYTYGKVPVGHVTVSICKRYS DASDCHGEDSQAFCEKFSG
	HP	SANFSFNDEEMKNVMDSSNGLSEY-LDLSFPGPVEILT TVTESVTG----ISRNVTNMF
		* * * * * * * * * *
20	MG	QLNSHGCFYQQVKTQVFLKRRKEYEMKLHTEAQIQEEGTVVELTGRQSSEITRTITKLSF
	HP	FK--QHDYIIIEFFDYTTVLKPSLNFTATVKVTRADGNQLTLEERRNNVITVTRNYTEY
		* * * * * * * * * *
	MG	VKVDSHFRQGIPFFGQVRLVDGKGVPIPNKVIFIRGN-----EANYYSNATDEHGLV
	HP	WSGNSGNQKMEAVQKINYTPQSGTFKIEFFILEDSSSELQKAYFLGSKSSMAVHSLFK
25		* * * * * * * * * *
	MG	QFSINTTN-VMGTSLTVRVNYKDRSPCYGYQWVSEEHEEAHHTAYLVFSPSKSFVHLEPM
	HP	S--PSKTYIQLKTRDENIKVGS PFELVVSGNKRKLKELSYMVVSRGQLVAVGKQ--NSTMF
		* * * * * * * * * *
	MG	SHELPCGHTQTVQAHYILNGGTLLGLKKLSFYLLIMAKGGIVRTGTHGLLVKQEDMKGHF
30	HP	S-LTPENS-WTPKACVIVYIIEDDGEIISDVLKIPVQLVFKNKIKLYWSKVKAEPSEKVS
		* * * * * * * * * *
	MG	SISIPVKSDIAPVARLLIYAVLPTGDVIGDSAKYDVENCLANKVDLSFSPSQSLPASHAH
	HP	LRISVT-QPDSIVGIVAVDKSVNLMNASNDITMENVVHEL-ELYNTG-----
		* * * * * * * * * *
35	MG	LR--VTAAPQSVCALRAVDQSVLLMKPDAELSASSVYNLLPEKDLTGFPGLNDQDDEDC

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HP -----YYLGMFMNSFAVFOE-CGLWVLTDANL---TKDYIDGVYDIAEYAEFRMEENEG
      * * * * *
MG INRHNVYINGITYTPVSSSTNEKDMYSFLEDMGGLKAFNTSKIRKPKMCPQLQQYEMHGPEG
HP HIV-----DIHDFSLGSSPH---VRKHPFETWIWLDTNMGSRITYQEFEVTVPDSI
5      * * * * *
MG LRVGFYESDVMGRGHARLVHVEEPTETVRKYFPETWIWDLVVVNSAGVAEVGVTVPDTI
HP TSWVATGFVISEDGLGLTTTPVELQAFQPFIFLNLPSVIRGEEFALEITIFNYLKDA
      * * * * *
MG TEWKAGAFCLSEDAGLGISST-ASLRAFQPPFVELTMPYSVIRGEAFTLKATVLNLYPKC
10 HP TEVKVIEKSDKFDILMTSSE-----INATGHQ-QTLLVPSSEDGATVLFPIRPHL--GE
      * * * * *
MG IRVSVQLEASPAFLAVPVEKEQAPHICANGRQTVSWAVTPKSLGNVNFTVSAEALSEQE
HP IPITVTALSP--TASDAITQMILVKAEGIEKSYSQSILLDLTDNRLQSTLKTLSFSFPNN
      * * * * *
15 MG LCGTEVPSVPEHGRKDTVIKPLLVEPEGLEKETTFNSLL---CPSGGEVSEELSLKLPPN
HP TVTGSEVRQITAIGDVLGPSINGLASLIRMPYGCGEQNMINFAPNIYILDYLTKKKQLTD
      * * * * *
MG VVEESARASVSVLGDILGSAMQNTQNLLOMPYGCGEQNMVLFAPNIYVLDYLNQQLTP
HP NLKEKALSFMROGYQRELLYQREDGSFSAFG--NYDPSGSTWLSAFVLRFCLEADPYIDI
20      * * * * *
MG EVKSKAIGYLNTRYQRLNYKHYDGSYSTFGERYGRNQGNWTWLTAFVLKTFQAQARAYIFI
HP DQNVLHRTYTWLKGHQKSNGEFWDPRVHSELQGGNKSPVTLTAYIVTSLGLYRKYQPN
      * * * * *
MG DEAHITQALIWLSQRQKDNCGFRSSGSLNNAIKGGVEDEVTLISAYITIALLEIPLTVTH
25 HP IDVQESIHFLES-----EFSRGISDNYTLALITYALSSVG-SPKAKEALNMLTWRAEQE
      * * * * *
MG PVVRNALFCLESAWKTAQEGDHG-SHVYTKALLAYAFALAGNQDKRKEVLKSLNEEAVKK
HP GGMQFW-----VSSESKLSDSWQPRSLDIEVAAYALLSHFLQFQ--TSE----GIPIMRW
      * * * * *
30 MG DNSVHWERPQKPKAPVGHFYEPQAPSAEVEMTSYVLLAYLTAQPAPTSDELTSATNIVKW
HP LSRQRNSLGGFASTQDTTVALKALSEFAALMNTERTNIQVTVTGPS--PSPVKFLIDTHN
      * * * * *
MG ITKQONAQGGFSSTQDTVVALHALSKYGAATFT-RTGKAAQVTIQSSGTFSSKFQVDNNN
HP RLLQLTAELAVVQPTAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNEAFDLQVA
35      * * * * *

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MG RLLLQVSL-PELPGEYSMKVTGEGCVYLQTSLKYN----ILPEKEEFPFALGVQTLPQT
HP VKENK-DDLNHVLDLNVCTSFSGPGRSGMALMEVNLLSGFMVPSEAISSLSETVKKVEYDHG
      * *      * *      *      * * *      *      * * *      * *      * * *
MG CDEPKAHTSFQISLSVSYTGS-RSASNMAIVDKMVSGF-----IPLKPTVKMLE-----
5  HP KLNLYLDSVNETQFCVNIPAVRNFKVSNTQDASVSIVDYEP RRQAVRSYNSEVKLSSCD
      * *      *      * * *      *      *      * *      *
MG ----RSNHVS RTEVSSNHVLIYLDKVSNTLSLFFTVLQDVP----VR-----D
HP LCSDVQGCRCEDGASGSHHSSVIFIFCFKLLYFMELWL
      *      *      * * *
10 MG L---KPAIVKVYDYYETDEFAIAEYNAPCSKDL----GNA

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Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W33075) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

20

<HP02991> (SEQ ID NOS: 32, 42, and 52)

Determination of the whole base sequence of the cDNA insert of clone HP02991 obtained from cDNA library of human epidermoid carcinoma cell line KB revealed the structure consisting of a 81-bp 5'-untranslated region, a 1749-bp ORF, and a 800-bp 3'-untranslated region. The ORF encodes a protein consisting of 582 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 12 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 66 kDa that was somewhat larger than the molecular weight of 64,244 predicted from the ORF. In

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this case, the addition of a microsome led to the formation of a product of 78 kDa to which sugar chains are presumably attached. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from valine at position 27. In addition, there exist in the amino acid sequence of this protein seven sites at which N-glycosylation may occur (Asn-Gly-Thr at position 70, Asn-Gly-Thr at position 182, Asn-Gly-Ser at position 294, Asn-His-Thr at position 310, Asn-Gly-Thr at position 352, Asn-Glu-Thr at position 393 and Asn-Cys-Ser at position 407).

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the mouse FKBP65-binding protein (GenBank Accession No. L07063). Table 9 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the mouse FKBP65-binding protein (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 88.8% in the entire region.

Table 9

	HP	MFPAGPPSHSILRLPLQLLLLLVVQAVGRGLGRASPAGGPLEDVVIERYHIPRACPREVQ
		** .*.***. *...*.***** .*...*****.*****.*****
5	MM	MFLVGSSSHTLHRVRIPLLLL-LQTLERGLGRASPAGAPLEDVVIERYHIPRACPREVQ
	HP	MGDFVRYHYNGTFEDGKKFDSSYDRNTLVAIVVGVRITGMDRGLMGMVCNERRRLIVP
		*****.*****.*****.*****.*****.*****.*****.*****
	MM	MGDFVRYHYNGTFEDGKKFDSSYDRSTLVAIVVGVRITGMDRGLMGMVCNERRRLIVP
	HP	PHLGYGSIGLAGLIPPDATLYFDVLLDVWNKEDTVQVSTLLRPPHCPRMVQDGFVRYH
10		*****.*****.*****.*****.*****.*****.*****.*****
	MM	PHLGYGSIGVAGLIPPDATLYFDVLLDVWNKADTVQSTILLRPPYCPRMVQNSDFVRYH
	HP	YNGTLLDGTSTFDTSSYKGGTYDITYVSGWLIKGMQGLLGMCPGERRKIIIPPLAYGEK
		*****.***.***.*****.*****.*****.*****.*****
	MM	YNGTLLDGTGFDNSYSRGGTYDITYISGWLIKGMQGLLGMCPGERRKIIIPPLAYGEK
15	HP	GYGTVIPPQASLVFVLLIDVHNPKDAVQLETLELPQGCVRRAVAGDFMRYHYNGSLMDG
		*****.***.*****.*****.*****.*****.*****.*****
	MM	GYGTVIPPQASLVFVLLIDVHNPKDTVQLETLELPQGCVRRAVAGDFMRYHYNGSLMDG
	HP	TLFDSSYSRNHTYNTYIGQYIIPGMDQLQACMGERRRITIPPHLAYGENGTGDKIPG
		*****.*****.*****.*****.*****.*****.*****.*****
20	MM	TLFDSSYSRNHTYNTYVGQYIIPGMDQLQACIGERRRITVPPHLAYGENGTGDKIPG
	HP	SAVLIFNVHVIDFHNPAADVVEIRTLRPSSETCNETTKLGDFVRYHYNCSLLDGTQLFTSH
		*****.*****.* ***.*****.*.*****.*.***.*****.***.***
	MM	SAVLIFDVHVIDFHNPSDPVEIKTLRPPENCNETSKI GDFIRYHYNCSLLDGTRLFSSH
	HP	DYGAPQEATLGANKVIEGLDTGLQGMCGERRQLIVPPHLAGESGARGVPGSAVLLFEV
25		** .**** ***** *****.*****.*****.*****.*****
	MM	DYEAPQEITLGANKVIEGLDRGLQGMCGERRQLIVPPHLAGENGARGVPGSAVLLFEV
	HP	ELVSREDGLPTGYLFVWHKDPANLFDMDLNKDGEVPPEEFSTFIKAQVSEKGRMLPG
		*****.***.***.*****.*****.*****.*****.*****
	MM	ELVSREDGLPTGYLFVWYQDPSTSLFEDMDLNKDGEVPPEEFSSFIKAQVNEGKGRMLPG
30	HP	QDPEKTIGDMFQNDQDRNQDKITVDELKLKSDDEERVHEEL
		..*****.*****.*****.*****.*****
	MM	QDPDKTISDMFQNDQDRNQDKITAEELKLKSDDEQERVHEEL

sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA308536) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03063> (SEQ ID NOS: 33, 43, and 53)

Determination of the whole base sequence of the cDNA insert of clone HP03063 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 88-bp 5'-untranslated region, a 1233-bp ORF, and a 151-bp 3'-untranslated region. The ORF encodes a protein consisting of 410 amino acid residues and there existed a putative transmembrane domain at the N-terminus. Figure 13 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 46 kDa that was almost identical with the molecular weight of 45,786 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the mouse AUP1 (GenBank Accession No. U41736). Table 10 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the mouse AUP1 (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 90.2% in the entire region.

Table 10

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HP MELPSGPGPERLFDSHRLPGDCFLLLVLLLYAPVGFCLLVLRFLGLIHVFLVSCALPDSV
  ** * .*****.* ****.******.******.******
5 MM MEPPPAPGPERLFDSHRLPSDGFLLALLLYAPVGLCLLVLRFLGLHVLVSCALPDSV
HP LRRFVVRTMCAVLGLVARQEDSGLRDHSVRVLISNHVTPFDHNIVNLLTTCSTPLLNSPP
  *****.******.******.******.******.******
MM LRRFVVRTMCAVLGLVARQEDSGLRDHSVRVLISNHVTPFDHNIVNLLTTCSTPLLNSPP
HP SFVCWSRGFMEMNGRGELVESLKRFCASTRLPPTPLLLFPEEEATNGREGLLRFSSWPFS
10 *****.* *****.******.******.******.******
MM SFVCWSRGFMEMDRRVELVESLKRFCASTRLPPTPLLLFPEEEATNGREGLLRFSSWPFS
HP IQDVVQPLTLQVQRPLVSVTVSDASWVSELLWSLFPFTVYQVRWLRPVHRQLGEANEFF
  *****.******.******.******.******.******
MM IQDVVQPLTLQVQRPLVSVTVSDASWVSELLWSLFPFTVYQVRWLHPIRRQLGESEEF
15 HP ALRVQQLVAKELGQTGTRLTPADKAEHMKRQRHPRLRPQSAQSSFPSPGSPDVQLATL
  *****.******.******.******.******.******
MM ALRVQQLVAKELGQIGTRLTPADKAEHMKRQRHPRLRPQSVQSSFPSPSPSSDVQLTTL
HP AQRVKEVLPHVPLGVIQRDLAKTGCVDLTITNLLEGAVAFMPEDITKGTQSLPTASASKF
  *.*****.******.******.******.******.******
20 MM AHRVKEVLPHVPLNVIQRDLARTGCVDLTITNLLEGAVAFMPEDVTEGSQSPPAPSAPKF
HP PSSGPVTPQPTALTFAKSSWARQESLQERKQALYFYARRRFTERRAQEAD
  ****.******.******.******.******.******
MM PSSGLATPQPTALTFAKSSWARQESLQERKQALYFYARRRFRERQAQAE

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Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA131932) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

30

<HP03091> (SEQ ID NOS: 34, 44, and 54)

Determination of the whole base sequence of the cDNA insert of clone HP03091 obtained from cDNA library of human liver revealed the structure consisting of a 16-bp 5'-untranslated region, a 1452-bp ORF, and a 184-bp 3'-untranslated region. The ORF encodes a protein consisting of 483 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 14 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from leucine at position 34.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human OS-9 protein (SWISS-PROT Accession No. Q13438). Table 11 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human OS-9 protein (OS). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 27.8% in the N-terminal region of 281 amino acid residues. The positions of eight cysteines were conserved between the two proteins.

Table 11

20 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. AA313678) among ESTs. However, since
they are partial sequences, it can not be judged whether or
25 not they encode the same protein as the protein of the
present invention.

Determination of the whole base sequence of the cDNA
30 insert of clone HP03092 obtained from cDNA library of human
liver revealed the structure consisting of a 19-bp 5'-
untranslated region, a 1824-bp ORF, and a 269-bp 3'-
untranslated region. The ORF encodes a protein consisting of

607 amino acid residues and there existed at least six putative transmembrane domains. Figure 15 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro
5 translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the rat liver-specific transport
10 protein (GenBank Accession No. L27651). Table 12 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the rat liver-specific transport protein (RN). Therein, the marks of - and *
represent a gap and an amino acid residue identical with
15 that of the protein of the present invention, respectively. The both proteins shared a homology of 70.0% in the entire region.

Table 12

HP MGFEELLEQVGGFGPFQLRNVALLALPRVLLPLHFLLPIFLAAVPAHRCALPGAPANFSH

 5 RN MGFEDLLDKVGGFGPFQLRNLVLMALPRMLLPMHFLLPVFMAAVPAHHCALPGAPANLSH
 HP QDVWLEAHLPREPDGTLSSCLRFAYPQALPNTTLGEERQSRGELEDEPATVPCSQGWEYD

 RN QDLWLEAHLPRETDGSFSSCLRFAYPQTPVNVTLGTEVSNSGEPEGEPLTVPCSQGWEYD
 HP HSEFSSTIATESQVGIYIIHLEVECRWRQSPWEAAGRGLPWEEAEAAGLGRDKVSYSPSW
 10 *****
 RN RSEFSSTIAT-----
 HP RESLGGLSGMEWDLVCEQKGLNRAASTFFAGVLVGAVAFGYLSDRFGRRRLLLVAYVS

 RN -----EWDLVCQQRGLNKITSTCFFIGVLVGAVVYGYLSDRFGRRRLLLVAYVS
 15 HP TLVLGLASAASVSYVMFAITRILTGSALAGFTIIVMPLELEWLDVEHRTVAGVLSSTFWT

 RN SLVLGLMSAASINYIMFVVTRILTGSALAGFTIIVLPLELEWLDVEHRTVAGVISTVFW
 HP GGVMLLALVGYLIRDWRWLLAVTLPCAPGILSLWWVPESARWLLTQGHVKEAHRYLLHC

 20 RN GGVLLLALVGYLIRSWRWLLAATLPCVPGIISIWWVPESARWLLTQGRVEEAKKYLLSC
 HP ARLNGRPVCEDSFSQEA VSKVAAGERVVRRPSYLDLFRTPRLRHISLCCVVWFGVNFYSY

 RN AKLNGRPVGEGLSQAELNNVVTMERALQRPSYLDLFRTSQRLRHISLCCMMVWFGVNFYSY
 HP YGLSLDVSGGLNVYQTQLLFGAVELPSKLLVYLSVRYAGRRLTQAGTLLGTALAFGTRL
 25 *****
 RN YGLTLDVSGGLNVYQTQLLFGAVELPSKIMVYFLVRRLGRRLTEAGMLLGAALTFGTSL
 HP LVSSDMKSWSTVLAVMGKAFSEAAFTTAYLFTSELYPTVLRQTGMGLTALVGRLGGS LAP

 RN LVSLETKSWITLVVVGKAFSEAAFTTAYLFTSELYPTVLRQTGLGLTALMGRLGASLAR
 30 HP LAALLDGVWLSLPKLT YGGIALLAAGTALLLPETRQAQLPETIQDVERKSAPTSLQEEEM

 RN LAALLDGVWLLLPKVAYGGIALVA ACTALLLPETKKAQLPETIQDVERK----STQEE--
 HP PMKQVQN
 35 RN -----DV

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI016020) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03116> (SEQ ID NOS: 36, 46, and 56)

Determination of the whole base sequence of the cDNA insert of clone HP03116 obtained from cDNA library of human epidermoid carcinoma cell line KB revealed the structure consisting of a 32-bp 5'-untranslated region, a 945-bp ORF, and a 110-bp 3'-untranslated region. The ORF encodes a protein consisting of 314 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 16 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from lysine at position 20. In addition, there exist in the amino acid sequence of this protein three sites at which N-glycosylation may occur (Asn-Arg-Thr at position 167, Asn-Asn-Ser at position 200 and Asn-Ile-Ser at position 273).

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human Prostasin (SWISS-PROT Accession No. Q16651). Table 13 shows the comparison between amino acid sequences of the human protein of the present

invention (HP) and the human Prostasin (PR). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 39.8% in the entire region.

Table 13

10	HP	MGARGALLLALLLARAGLRKPESQEAPLSGPCGRRVITSRIVGGEDAELGRWPW
		..*.* . . * ** * . ***** . ***** *.*.*
	PR	MAQKGVLPQQLGAVAILLYLGLLRSGTG-AEGAEAPCG-VAPQARITGGSSAVAGQWPW
	HP	QGSRLWDSHVCGVSLLSHRWALTAAHCFETYSDLSDPGWMVQFGQLTSMPSFWSLQAY
		* * . ***** *.*.*.*.*.*.*.*.*.* *.*.* . * .
15	PR	QVSITYEGVHVCGLVSEQWVLSAAHCF---PSEHHKEAYEVKLGA-HQLDSY---SED
	HP	YTRYFVSNIYLSRYLGNSPY-DIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVT
	* *.*.* ... ***** *.*.*.*.*.*.*.*.*.* .. * * . * **
	PR	AKVSTLKDIIHPHPSYLQEGSQGDIALQLSRPITFSRYIRPICLPAANASFPNGLHCTVT
	HP	GWGYIKEDALPSPHTLQEVQVAIINNSMCNHLF-LKYSFRKDIF--GDMVCAGNAQGGK
20		****. . . * .*****..... ** * * .***** ..****
	PR	GWGHVAPSVSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEPHFVQEDMVCAGYVEGGK
	HP	DACFGDSGGPLACNKNGLWYQIGVVSWSGVCGRPNRPGVYTNIHHFEWIQKLMAQSGMS
		*** *****.* .***** .***** ** .***** * .***** ...
	PR	DACQGDGGPLSCPVEGLWYLTGIVSWGACGARNRPGVYTLASSYASWIQSKVTELQPR
25	HP	QPDPSWPLLFFPLLWALPLLGPV
	PR	VVPQTQESQPDNSNLCGSHLAFSSAPAQGLLRPILFLPLGLALGLLSPWLSEH

30 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA159101) among ESTs. However, since they are partial sequences, it can not be judged whether or

not they encode the same protein as the protein of the present invention.

<HP10618> (SEQ ID NOS: 37, 47, and 57)

5 Determination of the whole base sequence of the cDNA
insert of clone HP10618 obtained from cDNA library of human
fibrosarcoma cell line HT-1080 revealed the structure
consisting of a 215-bp 5'-untranslated region, a 285-bp ORF,
and a 1194-bp 3'-untranslated region. The ORF encodes a
10 protein consisting of 94 amino acid residues and there
existed a putative transmembrane domain at the N-terminus.
Figure 17 depicts the hydrophobicity/hydrophilicity profile,
obtained by the Kyte-Doolittle method, of the present
protein. In vitro translation resulted in formation of a
15 translation product of 10 kDa that was almost identical with
the molecular weight of 9,709 predicted from the ORF.

Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
20 example, Accession No. AA287125) among ESTs. However, since
they are partial sequences, it can not be judged whether or
not they encode the same protein as the protein of the
present invention.

25 <HP10619> (SEQ ID NOS: 38, 48, and 58)

Determination of the whole base sequence of the cDNA
insert of clone HP10619 obtained from cDNA library of the
human fibrosarcoma cell line HT-1080 revealed the structure
consisting of a 11-bp 5'-untranslated region, a 657-bp ORF,
30 and a 854-bp 3'-untranslated region. The ORF encodes a
protein consisting of 218 amino acid residues and there
existed a putative transmembrane domain at the N-terminus.

Figure 18 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

5 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. Z43089) among ESTs. However, since they are partial sequences, it can not be judged whether or
10 not they encode the same protein as the protein of the present invention.

<HP10622> (SEQ ID NOS: 39, 49, and 59)

 Determination of the whole base sequence of the cDNA
15 insert of clone HP10622 obtained from cDNA library of the human liver revealed the structure consisting of a 43-bp 5'-untranslated region, a 1383-bp ORF, and a 165-bp 3'-untranslated region. The ORF encodes a protein consisting of
20 460 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 19 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. Application of the (-3,-1) rule, a method for predicting the cleavage site of
25 the secretory signal sequence, allows to expect that the mature protein starts from serine at position 17. In addition, there exist in the amino acid sequence of this protein four sites at which N-glycosylation may occur (Asn-Ser-Ser at position 23, Asn-Met-Ser at position 115, Asn-Glu-Thr at position 296 and Asn-Tyr-Thr at position 357).

30 The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human angiopoietin-1 (GenBank

Accession No. U83508). Table 14 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human angiopoietin-1 (AN). Therein, the marks of -, *, and . represent a gap, an amino acid
5 residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 28.2% in the entire region and a homology of 39.1% in the C-terminal region of 215 amino
10 acid residues.

Table 14

HP	MFTIKLLLFIVPLVISS
5	AN MTVFLSFAFLAAILTHIGCSNQRRSPENSGRRYNRIQHGCAYTFILPEHDGNCRESTTD HP RIDQDNSSFDSLSPKSRFAMLDVVKILANGLLQLGHGLKDF-VHRTKGQINDIFQKLN ** . . . * * . . . * . . . * . . . * . . .
10	AN QYNTNALQRDAPHVEPDFSSQKLQHLEHVMENYTQWLQKLENYIVENMKSEMAQI-QQNA HP IFDQSPFYDLSLQTSSEIKKEEKEELRR-TTYKLQVKNEEVKNMSLELNSKLESILLEEKILLQ * . . . * * . . . * . . . * . . . * . . . * . . . * . . . AN VQNHATATMLEIGTSLLSQTAEQTRKLTQVETQVLNQTSLRLEIQLENSLSTYKLEKQLLQ HP QKVKYLE-EQLTNLIQNQPETPEHPEVTSKTFVEKQDNSIKDLLQTVEDQYKQLNQQHS * . . * . . . * * . . . * . . . * . . . * . . . * . . . * . . .
15	AN QTNEILKIHEKNSLLEHKILEMEGKHKEELDTLKEEKEN-LQGLVTRQTYIIQELEKQLN HP QIKEIENQLRRTSIQEPTEISLSSKPRAPRTTPFLQNEIRNVKHDGIPAECTTIYNRGE * . . . * * * * * AN RATNNSVLQKQQL-ELMDTVHNLVNLCCKEGLV--KGGKREEEKPFR-DCADVYQAGF HP HTSGMYAIRPSN-SQVFHVYCDV-ISGSPWTLIQHRIDGSQNFNETWENYKYGFGRLDGE * . . . * * * * *
20	AN NKSGIYTIYINNMEPKKVFENMDVNGGGWTVIQHREDGSLDFQRGWKEYKMGFGNPSGE HP FWLGLEKIYSIVKQSNYVLRIELEDWKDNKHYIEY-SFYLGNHETNYTLHLVAITGNVNP * . . . * * * * * AN YWLGNEFIFAITSQRQYMLRIELMDWEGNRAYSQYDRFHIGNEKQNYRLYLKGTGTAGK HP AIP-ENKDLVFSTWDHKAAGHF-NCPEGYSGGWWHDECENNLNGKYNKPRAKSKPERR * . . . * * * * *
25	AN QSSLILHGADFSTKDADNDNCMCKCALMLTGGWWF-DACGPSNLNGMFY--TAGQNHGKL HP RGLSWKSQNGRLYSIKSTKMLIHPTDSESE * . . . * * * * *
30	AN NGIKWHYFKGPSYSLRSTTMMIRPLDF

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for

example, Accession No. R86161) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

5

<HP10625> (SEQ ID NOS: 40, 50, and 60)

Determination of the whole base sequence of the cDNA insert of clone HP10625 obtained from cDNA library of the human liver revealed the structure consisting of a 133-bp
10 5'-untranslated region, a 651-bp ORF, and a 465-bp 3'-untranslated region. The ORF encodes a protein consisting of 216 amino acid residues and there existed two putative transmembrane domains. Figure 20 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-
15 Doolittle method, of the present protein.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R59052) among ESTs. However, since
20 they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP02883> (SEQ ID NOS: 61, 71, and 81)

25 Determination of the whole base sequence of the cDNA insert of clone HP02883 obtained from cDNA library of human epidermoid carcinoma cell line KB revealed the structure consisting of a 191-bp 5'-untranslated region, a 1179-bp ORF, and a 2657-bp 3'-untranslated region. The ORF encodes a
30 protein consisting of 392 amino acid residues and there existed three putative transmembrane domains. Figure 21 depicts the hydrophobicity/hydrophilicity profile, obtained

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for
5 example, Accession No. F11409) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

10 <HP03140> (SEQ ID NOS: 62, 72, and 82)

Determination of the whole base sequence of the cDNA insert of clone HP03140 obtained from cDNA library of human
fibrosarcoma cell line HT-1080 revealed the structure consisting of a 29-bp 5'-untranslated region, a 1494-bp ORF,
15 and a 972-bp 3'-untranslated region. The ORF encodes a protein consisting of 497 amino acid residues and there existed one putative transmembrane domain. Figure 22 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro
20 translation resulted in formation of a translation product of 51 kDa that was almost identical with the molecular weight of 54,245 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the
25 protein was similar to the *Caenorhabditis elegans* hypothetical protein CELC50D2 (GenBank Accession No. AF040642). Table 16 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *Caenorhabditis elegans* hypothetical protein CELC50D2
30 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that

of the protein of the present invention, respectively. The both proteins shared a homology of 37.9% in the N-terminal region of 393 amino acid residues.

5

Table 16

	HP	MALWRGSAYAGFLALAVGCVFLLEPELPGSALRSLWSSICLGPAPAPPGVSPPEGR	LAAA
			* * . . .
	CE	MFSETFVPSIFSYKHRLLHLSVLEFFIVPYWYSYNDQHRLSSYSVETAMFLS	
10	HP	WDALIVRPVRRWRRVAVGVNACVDVVLSGVKLLQALGLSPGNGKDHSLHSRNDLEEAFI	
		*. *. * * * * * * *	
	CE	WERAIVKPGAMFKKAVIGFNCNVDLIVSGVRVVDALNTTCSEKDKQETLETADLHQTF	A
	HP	HFMWKGAAAERFFSDKETFDIAQVASEFPGAQHYVGGNAALIGQKFAAN-SDLKVL	LCG
		*. * * * * *	
15	CE	HFFQRGAAAERYMSSSEDQFNLLVAESEASTRSHHHIGGNAALMADRIAANFPSTE	VYLVG
	HP	PVGPRLHELDDNVFVPPELQEVDEFHLILEYQAGEEWGQLKAPHANRFIFSHDLS	NGA
		*. * * * * * *	
	CE	PIGPRSQALLHPSVKRTNSTRILKDELHVILEYKQGEILGDWVAPSSSRFITSHD	HFGS
	HP	MNMLEVFVSSLEEFQPDLVVLSGLHMEGQSKELQRKRLEVVTSISDIPTGIPVH	LELA
20		* * * * * *	
	CE	MVVMEMFFKAIQFRPDLVVITGVHLLFQSKEMRQEKMRLLIKRNLQIPPKVPIH	LELG
	HP	SMTNRELMSSIVHQQVFPVAVTSLGLNEQELLFLTQSASGPH-SSLSSWNGVPD	VGMVSDI
		* * * * * *	
	CE	SLAD-EIFSTDVINKILPYVDSLGINEQELTFLSHIANGPHMEEYPVQAGTVH	VHKVEM
25	HP	LFWILKEHGR-----SKSRASDLTRIHFHTLVYHILATVDGHWANQLAAVA	AAGARVAGT
		* * * * * * *	
	CE	LHWLLKTYGRDPTGQIASKTGYRLSRIHFHCLTYHIMVSSGTDWSNLAAGLA	AGARIAGR
	HP	QAC--ATETIDTSRVSLRAPQEFMTSHSEAGSRIVLNPKNPVVEWHREGISF	HFTPVLC
		* * * * * *	
30	CE	LSCNIGANTMDSELLEIRTPANFVLDKKIEKNYQFEAHKYMLTPFNIA	RCS
	HP	KDPIRTVGLGDAISAEGLFYSEVHPHY	
	CE	GGGILDEGVTFSDVHNVI	LNPTTRL

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA356000) among ESTs. However, since
5 they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10628> (SEQ ID NOS: 63, 73, and 83)

10 Determination of the whole base sequence of the cDNA insert of clone HP10628 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 66-bp 5'-untranslated region, a 1254-bp ORF, and a 297-bp 3'-untranslated region. The ORF encodes a
15 protein consisting of 417 amino acid residues and there existed four putative transmembrane domains. Figure 23 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation
20 product of 46 kDa that was almost identical with the molecular weight of 45,461 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Schistosoma mansoni* ATP-cassette
25 family protein (GenBank Accession No. L26286). Table 17 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *Schistosoma mansoni* ATP-cassette family protein (SM). Therein, the marks of -, *, and . represent a gap, an amino
30 acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The

both proteins shared a homology of 39.5% in the C-terminal region of 294 amino acid residues.

Table 17

[illegible]

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. U66688) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10629> (SEQ ID NOS: 64, 74, and 84)

Determination of the whole base sequence of the cDNA insert of clone HP10629 obtained from cDNA library of human retinoblastoma cell line WERI-RB revealed the structure consisting of a 259-bp 5'-untranslated region, a 1950-bp ORF, and a 1060-bp 3'-untranslated region. The ORF encodes a protein consisting of 649 amino acid residues and there existed at least eight putative transmembrane domains. Figure 24 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein CELF38B6 (GenBank Accession No. U40060). Table 18 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *Caenorhabditis elegans* hypothetical protein CELF38B6 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 39.1% in the C-terminal region of 445 amino acid residues.

HP MIPNQHNAGAGSHQPAVFRMAVLDTDLHILPSSVLPPFWKLVGVSVAIVCFARSYDGO
CE MKYAEINVNSGKHFRNLNYKLHETS
5 HP FVFDSEAIVNNKVAGVVGRADLLCALFFLLSFLGYCKAFRESNKEGAHSSTFWVLLSIF
CE TLGYHVVNIIICHTVATLVFYKLGKQLEHIFDFFNIAFSASILFAVHPVHTEAVANITGRA
HP LGAVAMLCKEQGITVLGLNAVFDILVIGKFNVLIVQKVLHKDKSLENLGMRLNNGLLFR
CE ELLMTIFSLAALILHVKNREINCKFVLLVILSTLSKEQGLMTIPIAICIDFLAHRSCRSN
HP MTLTSGGAGMLYVRWRIMGTGPPAFTEVDNPASFADSMVRAVNYNYYYYSLNAWLLLCF
10* .. * ... **..***..* ..* ..*..* ..*..* ..*
CE FVRMICLLVAIGFLRMVNGFEAAKFTKLDNPTAFLNSKFYRMINYTYIWLYHAYLLVIP
HP WWLCFDWSMGCIPLIKSISDWRVIALAALWFCILIGLICQALCEDGHKRRILTLGLGFLV
.....*..*..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..*
CE VNLCFDYSMGCISSITM--WDLRALSPVLIFTIVIIGVKF----QNECRAFTLSSLMGI
15 HP IPFLPASNLFFRVGFVVAERVLVYLPISIGYCVLLTFGFGALSKHTKKKKLIAAVVLGILFI
....*..*..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..*
CE ISFLPASNIFFTVGFSIAERVLVYLPISAGFCILCAIIFKKLSVHFKNADVLSITLILLIS
HP NTLRCVLRSGEWRSEEQLFRSALSVCPLNAKVHYNIGKNLADKGNQTAAIRYYREAVRLN
* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..*
20 CE KTYR---RSGEWKTELSLYSSGLSVCPTNAKIHYNLGKVLGDNGLTKDAEKYWNAIKLD
HP PKYVHAMNNGNIIKERNELQEAELLSLAVQIQPDFAAWMNLGIVQNSLKRFEAAEQS
.. ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..*
CE PSYEQALNNLGNLLEKSGDSKTAESLLARAVTLRPSFAVAMNGLISQMNLKKYYEAEKS
HP YRTAIKRRKYPDCYYNLGRLYADLNRHVDALNAWRNATVLKPEHSLAWNMIILLDNTG
25* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..*
CE LKNSLLIRPNSAHCLFNLGVLYQRTNRDEMAMSAWKNA TRIDPSHSQSWTNLFVVDHLS
HP NLAQAEAVGREALELIPNDHSLMFSIANVLGKSQKYKESEALFLKAIKANPNAASYHGNL
* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..*
CE QCSQVIDLSYQALSSVPNESRVHMQIGSCHAKHSNFTAENHIKSAIDLNPSTSVLFHANL
30 HP AVLYHRWGHLDLAKKHYEISLQLDPTASGTKENYGLLRKLELMQKAV
....* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..* ..*
CE GILYORMSRHKEAESQYRIVLALDSKNIVAKONLOKLEHNHCYNSTLP

35 Furthermore, the search of the GenBank using the bas

sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA450191) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10635> (SEQ ID NOS: 65, 75, and 85)

Determination of the whole base sequence of the cDNA insert of clone HP10635 obtained from cDNA library of human retinoblastoma cell line WERI-RB revealed the structure consisting of a 65-bp 5'-untranslated region, a 282-bp ORF, and a 111-bp 3'-untranslated region. The ORF encodes a protein consisting of 93 amino acid residues and there existed two putative transmembrane domains. Figure 25 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 10 kDa that was almost identical with the molecular weight of 9,489 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA516481) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10636> (SEQ ID NOS: 66, 76, and 86)

Determination of the whole base sequence of the cDNA insert of clone HP10636 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure

consisting of a 179-bp 5'-untranslated region, a 1278-bp ORF, and a 255-bp 3'-untranslated region. The ORF encodes a protein consisting of 425 amino acid residues and there existed ten putative transmembrane domains. Figure 26
5 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

Furthermore, the search of the GenBank using the base
10 sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. Z43270) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the
15 present invention.

<HP10640> (SEQ ID NOS: 67, 77, and 87)

Determination of the whole base sequence of the cDNA insert of clone HP10640 obtained from cDNA library of human
20 retinoblastoma cell line WERI-RB revealed the structure consisting of a 52-bp 5'-untranslated region, a 450-bp ORF, and a 553-bp 3'-untranslated region. The ORF encodes a protein consisting of 149 amino acid residues and there existed at least two putative transmembrane domains. Figure
25 27 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 17 kDa that was almost identical with the molecular weight of 16,829 predicted from the ORF.

30 The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Arabidopsis thaliana* hypothetical

protein F27F23.14 (GenBank Accession No. AC003058). Table 19 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the Arabidopsis thaliana hypothetical protein F27F23.14 (AT).
 5 Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 46.5% in the entire
 10 region other than the N-terminal region.

Table 19

	HP	METLYRVPFLVLECPNLKLLKPPWLHMPSTVYA
15		*** * *.*** *. . .***.*****
	AT	MAPRSDSQTGSSVSDGSDQSSMDPIFHLLRIVPFSFLRPPRLRLKIPS-FTLPSPMTVYA
	HP	LVVVSYFLITGGIYDVIVEPPSVGSMTD-EHGHQRPVAFLAYRVNGQYIMEGLASSFLF
	*.....*.....*.....*.....*.....*.....*.....*
	AT	LILLTYFLVSGFVDVIVEPPGIGSTQDPTTGTIRPVVFMSGRVNGQYIIEGLSSGFMF
20	HP	TMGGLGFIILDRSNAPNIPKLNRFLLLFIGFVCVLLSFFMARVFMRMKLPGYLMG
		..***.***.***. . . * . * . * *.....*.....*.....*
	AT	VLGGIGIVMLDLALDKNKAKSVKASYAVAGVSSIVIAYVMSMLFIRIKIPGYLY

25 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. N34717) among ESTs. However, since they are partial sequences, it can not be judged whether or
 30 not they encode the same protein as the protein of the present invention.

<HP10644> (SEQ ID NOS: 68, 78, and 88)

Determination of the whole base sequence of the cDNA insert of clone HP10644 obtained from cDNA library of the human retinoblastoma cell line WERI-RB revealed the structure consisting of a 221-bp 5'-untranslated region, a
5 1191-bp ORF, and a 204-bp 3'-untranslated region. The ORF encodes a protein consisting of 396 amino acid residues and there existed two putative transmembrane domains. Figure 28 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

10 The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein B0511.8 (GenBank Accession No. AF067608). Table 20 shows the comparison between amino acid
15 sequences of the human protein of the present invention (HS) and the *Caenorhabditis elegans* hypothetical protein B0511.8 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that
20 of the protein of the present invention, respectively. The both proteins shared a homology of 31.3% in the region of 361 amino acid residues other than the N-terminal region and the C-terminal region.

Table 20

	HS	MAMIELGFGRQNFHPLKRKSSILLKL
	CE	CDKNGQYLSVQEEIDAENKVQRKIAPGLNEKVLERVTOMLMKQEKSTETMYIWLKNLRVP
5	HS	IAVVFVAVLLFCEFLIYYLAIFQCNWPEVKTTASDGEQTTREPVLKAMFLADTHLLGEFLG
		* *..*...* .*** * .***...*****.. *
	CE	ILLAILLVYNEYFIFFIASFSCQWP-----CKYGRCS-ESSVKAFMISDTHLLGKING
	HS	HWLDKLRREWQMERAFQTALWLLQPEVVFILGDIFDEGKWSTPEAWADDVERFQKMFHRP
		*****.***** ..* ..* . *..*..*..*****... .. .***.*..*
10	CE	HWLDKLRREWQMYQSFWISTWIHSPDVTFFLGLDLMDEGKWAGRPVFEAYAERFKKLF--G
	HS	SHVQLKVVAGNHDIGFHYEMNTYKVERFEKVFSSERLFSWKGINFVMVNSVALNGDGCIGI
	 *****.*****. *..*.. .. . *..* ..*
	CE	DNEKVITLAGNHDLGPHYAL----VQTFATHLTPT--VELKNYLLIMPETLEMFKKEFRR
	HS	CSETEAELIEVSHRLNCSREARG-SSR-CGPGPL-----LPTSAPVLLQHYPLYRRS
15		. * * *.. . * ..* * . * ..* ..*..*****.*..*
	CE	GLIDEMKIKKHRFVLINSMAMHGDGCRLCHEAELILEKIKSRNPKNRPIVLQHFPLYRKS
	HS	DANCSGEDAAPAEERDIPFKENYDVLVSREASQKLLWWLQPRVLVSGHTHSAC-----EVH
		.*. *....*..*..*..*..* .. . *..* ..*..***. * ..
	CE	DAECDQVDEQHEIDLKEMYREQWDTLSKESLQIIDSLNPKAVFGGHTHKMCKKKWKNKTG
20	HS	HGGRVPPELSVPSFSWRNRNPNPSFIMGSIPTDYTLISKCYLPREDVVLIIYC-GVVGFLV
		... * . * ***** . *.... *.. ..*..* ..*..** * ..*..*
	CE	NSEYFYEYTVNSFSWRNGDVPAMLLVVIDGDNVLVSSCRLPSEILQIMVYIFGGIGILAK
	HS	LTLTHFGLLASPFLSGLNLLGKRKTR
25	CE	MYNDLITPAPLEWNVNNIAVCTAILVMIINVVALIFTIFWCLRSKDEGGEIDSNGGVIN

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R88381) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10656> (SEQ ID NOS: 69, 79, and 89)

Determination of the whole base sequence of the cDNA insert of clone HP10656 obtained from cDNA library of the human lymphoma cell line U937 revealed the structure consisting of a 68-bp 5'-untranslated region, a 1053-bp ORF, and a 739-bp 3'-untranslated region. The ORF encodes a protein consisting of 350 amino acid residues and there existed two putative transmembrane domains. Figure 29 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 41 kDa that was almost identical with the molecular weight of 40,043 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 54 kDa to which sugar chains are presumably attached. In addition, there exist in the amino acid sequence of this protein four sites at which N-glycosylation may occur (Asn-Cys-Thr at position 148, Asn-Tyr-Thr at position 155, Asn-Gln-Thr at position 162 and Asn-Lys-Ser at position 190).

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA917816) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10672> (SEQ ID NOS: 70, 80, and 90)

Determination of the whole base sequence of the cDNA insert of clone HP10672 obtained from cDNA library of the

human thymus revealed the structure consisting of a 244-bp 5'-untranslated region, a 462-bp ORF, and a 77-bp 3'-untranslated region. The ORF encodes a protein consisting of 153 amino acid residues and there existed a putative
5 secretory signal at the N-terminus and one putative transmembrane domain at the C-terminus. Figure 30 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. When expressed in COS cells, a product of 17 kDa was observed in
10 the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. N48700) among ESTs. However, since
15 they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03194> (SEQ ID NOS: 91, 101, and 111)

20 Determination of the whole base sequence of the cDNA insert of clone HP03194 obtained from cDNA library of human epidermoid carcinoma cell line KB revealed the structure consisting of a 120-bp 5'-untranslated region, a 912-bp ORF, and a 2406-bp 3'-untranslated region. The ORF encodes a
25 protein consisting of 303 amino acid residues and there existed four putative transmembrane domains. Figure 31 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation
30 product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the

protein was similar to the mouse hyperpolarization-activated cation channel HAC3 (GenBank Accession No. AJ225124). Table 21 shows the comparison between amino acid sequences of the human protein of the present invention (HS) and the mouse hyperpolarization-activated cation channel HAC3 (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 92.5% in the N-terminal region of 293 amino acid residues.

Table 21

15	HS MEAEQRPAAGASEGATPGLEAVPPVAPPPATAASGPIPKSGPEPKRRHLGTLLQPTVNKF *.*,*****.*.***. *. **,*,* * *** .*,*,*****.***** MM MEEEARPAAGAGEAATPARET-PPAAPAQARAASGGVPESAPEPKRRQLGTLLQPTVNKF HS SLRVFGSHKAVEIEQERVKSAGAWIIHPYSDFRFYWDLIMLLLMVGNLIVLPVGITFFKE *****
20	MM SLRVFGSHKAVEIEQERVKSAGAWIIHPYSDFRFYWDLIMLLLMVGNLIVLPVGITFFKE HS ENSPPWIVFNVLSDTFFLLDLVLNFRGTGIVVEEGAEILLAPRAIRTRYLRTWFLVDLISS ***** MM ENSPPWIVFNVLSDTFFLLDLVLNFRGTGIVVEEGAEILLAPRAIRTRYLRTWFLVDLISS HS IPVDYIFLVVELEPRLDAEVYKTARALRIVRFTKILSLLRLLRLSRLIRYIHWEEIFHM *****
25	MM IPVDYIFLVVELEPRLDAEVYKTARALRIVRFTKILSLLRLLRLSRLIRYIHWEEIFHM HS TYDLASAVVRIFNLIGMMLLLCHWDGCLQFLVPMQLQDFPPDCWVSINHMVVRSPHSSAFP *****.*.***.* MM TYDLASAVVRIFNLIGMMLLLCHWDGCLQFLVPMQLQDFPSDCWVSMNRMVNHWSGRQYSH
30	HS GPS MM ALFKAMSHMLCIGYGQAPVGMPPDVWLTMLSMIVGATCYAMFIGHATALIQSLDSSRRQY

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI571225) among ESTs. However, since
5 they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03219> (SEQ ID NOS: 92, 102, and 112)

10 Determination of the whole base sequence of the cDNA insert of clone HP03219 obtained from cDNA library of human lymphoma cell line U937 revealed the structure consisting of a 55-bp 5'-untranslated region, a 852-bp ORF, and a 237-bp 3'-untranslated region. The ORF encodes a protein consisting
15 of 283 amino acid residues and there existed four putative transmembrane domains. Figure 32 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product
20 of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human putative membrane protein 54TmP (GenBank Accession No. AF004876). Table 22 shows the
25 comparison between amino acid sequences of the human protein of the present invention (HS) and the human putative membrane protein 54TmP (TM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino
30 acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 56.5% in the entire region.

Table 22

[illegible]

Furthermore, the search of the GenBank using the base
25 sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. H86659) among ESTs. However, since
they are partial sequences, it can not be judged whether or
not they encode the same protein as the protein of the
30 present invention.

<HP03236> (SEQ ID NOS: 93, 103, and 113)

Determination of the whole base sequence of the cDNA insert of clone HP03236 obtained from cDNA library of human

fibrosarcoma cell line HT-1080 revealed the structure consisting of a 252-bp 5'-untranslated region, a 1467-bp ORF, and a 620-bp 3'-untranslated region. The ORF encodes a protein consisting of 488 amino acid residues and there
5 existed seven putative transmembrane domains. Figure 33 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

10 The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein ZC513.5 (GenBank Accession No. U53155). Table 23 shows the comparison between amino acid sequences
15 of the human protein of the present invention (HS) and the *Caenorhabditis elegans* hypothetical protein ZC513.5 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that
20 of the protein of the present invention, respectively. The both proteins shared a homology of 39.5% in the intermediate region of 365 amino acid residues.

Table 23

[illegible]

25

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA744858) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

30

<HP03237> (SEQ ID NOS: 94, 104, and 114)

Determination of the whole base sequence of the cDNA insert of clone HP03237 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 101-bp 5'-untranslated region, a 549-bp ORF, and a 1106-bp 3'-untranslated region. The ORF encodes a protein consisting of 182 amino acid residues and there existed four putative transmembrane domains. Figure 34 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human intestinal membrane A4 protein (SWISS-PROT Accession No. Q04941). Table 24 shows the comparison between amino acid sequences of the human protein of the present invention (HS) and the human intestinal membrane A4 protein (IM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 32.4% in the intermediate region of 111 amino acid residues.

Table 24

```

HS MWPPDPDPDPDPEPAGGSRPGPAVPGRLRALLPARAFLCSLKGRIILAEGLSFITFCYV
                                     ** **.* ** *.....**
5  IM                               MADSERLSAPGCWAACNFSRTRKGILLFAEIIILCLVILICF-
HS ASSASAFLTAPLLEFLLALYFLFADAMQLNDKWQGLCWPMMDFLRCVTAALIYFAISITA
   ..*..... . ...*..... * . . . . . * . . . . . ** **.* ..*.....* .***..
IM SASTPGYSSLSVIEMILAAIFFVVYMCDLHTKIPFINWPWSDFFRTLIAAILYLITSIVV
HS IAKYSDGASKAAGVFGFFATIVFATDFYLIFNDVAKFLKQGDSADETTAHKTEEENSDDSD
10 ... .. . . .***.....* . . * * . . .
IM LVERGNHISKIVAGVLGLIATCLFGYDAYVTFPVRQPRHTAAPTDPADGPV

```

Furthermore, the search of the GenBank using the base
 sequences of the present cDNA has revealed the registration
 of sequences that shared a homology of 90% or more (for
 example, Accession No. R14227) among ESTs. However, since
 they are partial sequences, it can not be judged whether or
 not they encode the same protein as the protein of the
 present invention.

<HP03267> (SEQ ID NOS: 95, 105, and 115)

Determination of the whole base sequence of the cDNA
 insert of clone HP03267 obtained from cDNA library of human
 liver revealed the structure consisting of a 148-bp 5'-
 untranslated region, a 555-bp ORF, and a 715-bp 3'-
 untranslated region. The ORF encodes a protein consisting of
 184 amino acid residues and there existed two putative
 transmembrane domains. Figure 35 depicts the
 hydrophobicity/hydrophilicity profile, obtained by the Kyte-
 Doolittle method, of the present protein. In vitro
 translation resulted in formation of a translation product
 of 21 kDa that was almost identical with the molecular

weight of 20,733 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human polyposis locus protein 1 (SWISS-PROT Accession No. Q00765). Table 25 shows the comparison between amino acid sequences of the human protein of the present invention (HS) and the human polyposis locus protein 1 (PL). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 59.1% in the entire region.

15

Table 25

	HS	MDGLRQ RVEHFLEQRNLVTEVLGALEAKTGVEKRYLAAGAVTLLSLYLLFGYGASLLCNL
		.*. *.....* .*. *. *****.....* *.....*.*****
	PL	MRERFDRFLHEKNCMTDLLAKLEAKTGVNRSFIALGVIGLVALYLVFGYGASLLCNL
20	HS	IGFVYPAYASIKAIESP SKDDTVWLTYWVVYALFGLAEFFSDLLSWFPFYVVGKCAFL
		*** *****. *.*** *****.....*****. *****. ***.***
	PL	IGFGYPAYISIKAIESP NKEDDTQWLTYWVVYGVFSIAEFFSDIFLSWFPFYMLKCGFL
	HS	LFCMAPRPWNGALMLYQVRVPLFLRHHGAVDRIMNDLSGRALDAAAGITRNVKPSQTPQ
		*.*****. * *** .***.*****.*****.....*.....*.....*
25	PL	LWCMAPSPSNGAELLYKRIIRPFPLKHESQMDSVVKDLKDKSKETADAITKEAKKATVNL
	HS	PKDK
	PL	LGEEKKST

30

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for

example, Accession No. R09702) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

5

<HP03270> (SEQ ID NOS: 96, 106, and 116)

Determination of the whole base sequence of the cDNA insert of clone HP03270 obtained from cDNA library of human lymphoma cell line U937 revealed the structure consisting of a 132-bp 5'-untranslated region, a 423-bp ORF, and a 656-bp 3'-untranslated region. The ORF encodes a protein consisting of 140 amino acid residues and there existed four putative transmembrane domains. Figure 36 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 17 kDa that was somewhat larger than the molecular weight of 15,864 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Schizosaccharomyces pombe* hypothetical protein (EMBL Accession No. AL031854). Table 26 shows the comparison between amino acid sequences of the human protein of the present invention (HS) and the *Schizosaccharomyces pombe* hypothetical protein (SP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 43.4% in the entire region.

Table 26

```

HS      MSRFLNVLRSWLVMVSIAMGNTLQSFDRDHTFLYEKLYTGKPNLVNGLQARTFGI
      ... .* *.**.* *. **.*** ... * ...* ...* **.***.***.*
5  SP MSQILAMLPDSLVAKWNVVVSVAALFNTVQSFLTPK-LTKRVY-SNTNEVNGLQGRTFGI
HS WTLSSVIRCLCAIDIHNKTLYHITLWTFLLALGHFLSELFVYGTAAPTIGVLAPIMVAS
      ***** ... ** .* * ... . *. ** ***** ... *... *.*.*.*.*
SP WTLSSAIVRFYCAYHITNPDVYFLCQCTYYLACFHLSEWLLFRTTNLGPGLLSPIVVST
HS FSILGMLVGLRYLEVEPVSRQKKRN
10      **
SP VSIWFMAKEKASILGIAA

```

Furthermore, the search of the GenBank using the base
 sequences of the present cDNA has revealed the registration
 of sequences that shared a homology of 90% or more (for
 example, Accession No. T30721) among ESTs. However, since
 they are partial sequences, it can not be judged whether or
 not they encode the same protein as the protein of the
 present invention.

<HP03298> (SEQ ID NOS: 97, 107, and 117)

Determination of the whole base sequence of the cDNA
 insert of clone HP03298 obtained from cDNA library of human
 lymphoma cell line U937 revealed the structure consisting of
 a 182-bp 5'-untranslated region, a 462-bp ORF, and a 455-bp
 3'-untranslated region. The ORF encodes a protein consisting
 of 153 amino acid residues and there existed at least one
 putative transmembrane domain. Figure 37 depicts the
 hydrophobicity/hydrophilicity profile, obtained by the Kyte-
 Doolittle method, of the present protein. In vitro
 translation resulted in formation of a translation product
 of 17.5 kDa that was almost identical with the molecular

weight of 17,360 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Schizosaccharomyces pombe* hypothetical protein SPBC119.09c (EMBL Accession No. AL022117). Table 27 shows the comparison between amino acid sequences of the human protein of the present invention (HS) and the *Schizosaccharomyces pombe* hypothetical protein SPBC119.09c (SP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 41.9% in the entire region other than the N-terminal region.

Table 27

HS	MNVGVAHSEVNPNTVRVMNSRGMWLTALGVGLLHIVLL
20	. * . * * *
SP	MGSSSSRRSSSLVTKVPKPTIDDRLDQGSATNYSNWVNYKGAWVIHIVLIAALRLIFH
HS	SIPFFSVFVAWTLTNIHNLGMYVFLHAVKGTPTFETPDQGKARLLTHWEQLDYGVOFTSS
	. ** * . ***** * * . ***** . . . * ** ***** * * . * . .
SP	AIPSVSRELAWTLTNLTVMAGSFIMFHWVTGTPFEFNGGAYDR-LTMWEQLDEGNQYTPA
25	HS RKFFTISPIILYFLASFYTKYDPHTFILNTASLLSVLIPKMPQLHGVRIFGINKY
	** . . ***** . ** . * * . ***** . * . ***** . *
SP	RKYLVLPIILFLMSTHYTHYNGWMFLVNIWALFMVLIPKLPVHRKRIFGIQKLSLRDD

30 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA043039) among ESTs. However, since

they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

5 <HP10631> (SEQ ID NOS: 98, 108, and 118)

Determination of the whole base sequence of the cDNA insert of clone HP10631 obtained from cDNA library of the human retinoblastoma cell line WERI-RB revealed the structure consisting of a 226-bp 5'-untranslated region, a
10 522-bp ORF, and a 2741-bp 3'-untranslated region. The ORF encodes a protein consisting of 173 amino acid residues and there existed one putative transmembrane domain. Figure 38 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

15 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W26443) among ESTs. However, since they are partial sequences, it can not be judged whether or
20 not they encode the same protein as the protein of the present invention.

<HP10658> (SEQ ID NOS: 99, 109, and 119)

Determination of the whole base sequence of the cDNA
25 insert of clone HP10658 obtained from cDNA library of the human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 24-bp 5'-untranslated region, a 228-bp ORF, and a 679-bp 3'-untranslated region. The ORF encodes a protein consisting of 75 amino acid residues and there
30 existed two putative transmembrane domains. Figure 39 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In

vitro translation resulted in formation of a translation product of 14 kDa or less that was almost identical with the molecular weight of 8,625 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T85006) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10663> (SEQ ID NOS: 100, 110, and 120)

Determination of the whole base sequence of the cDNA insert of clone HP10663 obtained from cDNA library of the human lymphoma cell line U937 revealed the structure consisting of a 67-bp 5'-untranslated region, a 480-bp ORF, and a 576-bp 3'-untranslated region. The ORF encodes a protein consisting of 159 amino acid residues and there existed two putative transmembrane domains. Figure 40 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA336522) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03165> (SEQ ID NOS: 121, 131, and 141)

Determination of the whole base sequence of the cDNA insert of clone HP03165 obtained from cDNA library of human

epidermoid carcinoma cell line KB revealed the structure consisting of a 128-bp 5'-untranslated region, a 1911-bp ORF, and a 1195-bp 3'-untranslated region. The ORF encodes a protein consisting of 636 amino acid residues and there
5 existed a putative secretory signal at the N-terminus. Figure 41 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 61 kDa that was smaller than the
10 molecular weight of 72,033 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from serine at position 33.

15 The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human β -galactosidase (GenBank Protein ID No. AAA51822). Table 28 shows the comparison between amino acid sequences of the human protein of the
20 present invention (HP) and the human β -galactosidase (GL). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The
25 both proteins shared a homology of 37.8% in the entire region.

HP MTTWSLRRRPARTLGLLLLVVGLFVLRRLDWSLTVPLRLRHLQGLQAKGNFMLEDST
 5 GL MPGFVLRILPLLLVLVLLLGPTRGRLNATQRMFEIDYSRDSFLKDGQP
 HP FWIFGGSIHYFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKDFDSGNLDLEAF
 * * * * *
 GL FRYISGSIHYSRVPFRFYWKDRLLKMKMAGLNAIQTYVPWNFHEPWGPQYQFSEDHDEVEYF
 HP VLMAAEIGLWVILRPGPYICSEMDLGGPLSWLLQDPGMRLRTTYKGFTAEVDLYFDHLS
 10 . . * * * * *
 GL LRLAHELGLLVILRPGPYICAEWEMGGPLPAWLLKESILLRSSDPDYLAADVKNLGVLLP
 HP RVVPLQYKRGGPPIAVQVENEYGSY--NKDPAYMPYVKKALEDR---GIVELLTSDNKDG
 . . * * * * *
 GL KMKPLLYQNGGPVITVQVENEYGSYFACDFDYLAFLQKRFRHHLGDDVVLFRTTDGAHKTF
 15 HP LSKGIVQGLATINLQSTHELQLLTFTFLF--NVQGTQPKVMMEYWTGWFDWSGGPHNILD
 * * * * *
 GL LKCGALQGLYTTVDFGTGSNIT--DAFLSQKCEPKGPLINSEFYTGWLDHWGQPHSTIK
 HP SSEVLKTVSAIVDAGSSINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDY
 * * * *
 20 GL TEAVASSLYDILARGASVNL YMFIGGTNFAYWNGA--NSPYAAQPTSYDYDAPLSEAGDL
 HP TAKYMKLRDFFGSISGIPLPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPIN
 * * * * *
 GL TEKYFALRNIIQKFEKVPEGPPIPPSTPKFAYGKVTLKLTVGAAILDILC-PSGPIK--S
 HP MENLPVNGGNGQSFGYILYETSI----TSSGILSGH---VHDRGQVFNVTVSIGFLDYKT
 25 * * * *
 GL LYPLTFIQVK-QHYGFVLYRTTLPQDCSNPAPLSSPLNGVHDRAYVAVDGIPQGVLE-RN
 HP TKIAVPLI-QGYTVLRILVENRGRVNYGENIDDQRKGLIGNLYLNDSPKLNFRYISL---
 * * * *
 GL NVITLNTGKAGATDLLVENMGRVNYGAYIND-FKGLVSNLTLSSNLTLDWTIFPLDTE
 30 HP DMKKSFFQRFG-----LDKWSSLPETPTLPAFFLGSLSI----SSTPCDTFLKLEGWE
 * * * * *
 GL DAVRSHLGGWGHRS GHHDEAWAHNSSNYTLPAFYMGNF SIPSGIPDLPDQDTFIQFPGWT
 HP KGVVFINGQNLGRYW-NIGPQKTLYLPGP-WLSSGINQVIVFEETMAGPALQFTETPHLG
 * * * * *
 35 GL KGOVWINGFNLGRYWPARGPOLTFVPOHILMTSAPNTITVLELEWAPCSSDDPELCAVT

HP RNQYIK

GL FVDRPVIGSSVTYDHPSKPFVEKRLMPPPPQKNKDSWLDHV

5

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA054017) among ESTs. However, since
10 they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03266> (SEQ ID NOS: 122, 132, and 142)

15

Determination of the whole base sequence of the cDNA insert of clone HP03266 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 69-bp 5'-untranslated region, a 957-bp ORF, and a 1464-bp 3'-untranslated region. The ORF encodes a
20 protein consisting of 318 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 42 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a
25 translation product of 34 kDa that was almost identical with the molecular weight of 35,363 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Arabidopsis thaliana putative
30 ribitol dehydrogenase (GenBank Protein ID No. AAC23625). Table 29 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the

Arabidopsis thaliana putative ribitol dehydrogenase (AT). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 39.0% in the region of 483 residues other than the N-terminal region.

Table 29

```

10      HP MVELMFPLLLLLLLPFLLYMAAPQIRKMLSSGVCTSTVQLPGKVVVVTGANTGIGKETAKE
                                         * . . . . . ** . . . . . * . . .
AT      MGIYGVMTGKKGKSGFGSASTAEDVTQOIDASHLTAIITGGTSGIGLEAARV
15      HP LAQRGARVYLACRDVEKGELVAKEIQTTTGNQQVLVRKLDLSDTKSIRAFAGFLAEKH
      ** * . . . * . * . . . . . * . . . * . . . . . * . . . * . . . * . . .
AT      LAMRGAHVIIAARNPKAANESKEMILQMNPNARVDYLQIDVSSIKSVRSFVDQFLALNVP
HP      LHLVINNAGVMMCPYSKTADGFEMHIGVNHGLGHFLLTHLLEKLEK-----ESAPSRIVNV
      * . . . . . * . . . . . * . . . * . . . . . * . . . . . * . . . * . . . . .
AT      LNILINNAGVMFCPFKLTEDGIESQFATNHIGHFLLTNLLLDKMKSTARESGVQGRIVNL
20      HP SSLAH---HLGRIHFHNLQGEKFYNAGLAYCHSKLANILFTQELARRLKGS--VTYYSV
      ** . . . * . . . . . * . . . * . . . . . * . . . . . * . . . * . . .
AT      SSIAHTYTYSEGIKFQGINDPAGYSERRAYGQSKLSNLLHSNALSRRLOEEGVNITINSV
HP      HPGTVQSELVRHSSFMRWWWLFSEF--FIKTPQQAQTSLHLCALTEGLEILSGNHFSCHV
      *** * . . . * . . . . . * . . . * . . . . . * . . . * . . . . .
25      AT HPGLVTTNLFRYSGFSMKVFRAMTFLFWKNIPQGAATTCYVALHPDLEGVTGKYFGDCNI
HP      AWVSAQARNETIARRLWDVSCDLLGLPID
      . * * * . . . * . . . * . . .
AT      VAPSKFATNNSLADKLWDFSFLIDSISK

```

30

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. D17020) among ESTs. However, since

they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

5 <HP03287> (SEQ ID NOS: 123, 133, and 143)

Determination of the whole base sequence of the cDNA insert of clone HP03287 obtained from cDNA library of human thymus revealed the structure consisting of a 83-bp 5'-untranslated region, a 249-bp ORF, and a 1133-bp 3'-untranslated region. The ORF encodes a protein consisting of 82 amino acid residues and there existed one putative transmembrane domain at the N-terminus and one at the C-terminus, respectively. Figure 43 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Schizosaccharomyces pombe* hypothetical protein 9.0kDa (SWISS-PROT Accession No. 013825). Table 30 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *Schizosaccharomyces pombe* hypothetical protein 9.0kDa (SP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 45.7% in the entire region.

Table 30

```

5  HP MAFTLYSLLQAALLCVNAIAVLHEERFLKNIGWGTDQGIGGFGE-EPGIKSQLMNLRISV
    ...*...*...*...*...*...*...*...*...*...*...*...*...*...*...*...
    SP MFGFGNILYVTLLLLNAVAILSEDRFLGRIGWSQSAAL-GFGDRQDTIKSRILHLIRAI
    HP RTVMRVPLIIVNSIAIVLLLLFG
    **** *...*...*...*...*...*...*...*...*...*...*...*...*...*...*...
    SP RTVMTFPLIAINTIVIVYNLVLG

```

10

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA853098) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10665> (SEQ ID NOS: 124, 134, and 144)

20 Determination of the whole base sequence of the cDNA insert of clone HP10665 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 31-bp 5'-untranslated region, a 744-bp ORF, and a 142-bp 3'-untranslated region. The ORF encodes a

25 protein consisting of 247 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 44 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a

30 translation product of 28 kDa that was somewhat larger than the molecular weight of 25,320 predicted from the ORF. In this case, the addition of a microsome led to the formation

of a product of 27 kDa. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from aspartic acid at position 26.

5 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA055367) among ESTs. However, since they are partial sequences, it can not be judged whether or
10 not they encode the same protein as the protein of the present invention.

<HP10669> (SEQ ID NOS: 125, 135, and 145)

15 Determination of the whole base sequence of the cDNA insert of clone HP10669 obtained from cDNA library of human retinoblastoma cell line WERI-RB revealed the structure consisting of a 73-bp 5'-untranslated region, a 621-bp ORF, and a 612-bp 3'-untranslated region. The ORF encodes a protein consisting of 206 amino acid residues and there
20 existed one putative transmembrane domain. Figure 45 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

25 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AF086533) among ESTs. However, since they are partial sequences, it can not be judged whether or
30 not they encode the same protein as the protein of the present invention.

<HP10670> (SEQ ID NOS: 126, 136, and 146)

Determination of the whole base sequence of the cDNA

insert of clone HP10670 obtained from cDNA library of human retinoblastoma cell line WERI-RB revealed the structure consisting of a 117-bp 5'-untranslated region, a 1299-bp ORF, and a 606-bp 3'-untranslated region. The ORF encodes a
5 protein consisting of 432 amino acid residues and there existed seven putative transmembrane domains. Figure 46 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

The search of the protein data base using the amino
10 acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein CELM03F8.2 (GenBank Protein ID No. AAB65910). Table 31 shows the comparison between amino acid sequences of the human protein of the present invention (HP)
15 and the *Caenorhabditis elegans* hypothetical protein CELM03F8.2 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention,
20 respectively. The both proteins shared a homology of 39.6% in the N-terminal region of 376 residues.

Table 31

```

HP MDARWWAVVLAAPFSLGAGGETPEAPPESWTQLWFFRVVNAAGYASFVPGYLLVQYF
. . . . . ** . . * . . . . ** . . * . . *
5 CE MDRSIMPIDSPARDKPPD--ELVWPLRLFLILLGYSTVATPAAILIYYV
HP RRKNYLETGRGLCFPLVKACVFGNEPKASDEVPLA---PRTEAAETTPMW-----QALKL
**... . . *... . . * . . . . * . . *... . . . . *
CE RRRNHAFETPYLSIRLLLS--FAVGNPEYQLIPTGEKQARKENDSIPQTRAQCINVIILL
HP LFCATGLQVSYLTWGVLQERVMTRSY--GATATSPGERFTDSQFLVLMNRVLALIVA--GL
10 ** .****. . *****.....* . . . . *.....* .....*
CE LFFFSGIQVTLVAMGVLQERIITRGYRRSDQLEVEDKFGETQFLIFCNRIVALVLSLMIL
HP SCVLCKQPRHGAPMYRYSFASLSNVLSSWCQYEALKFVSFPTQVLAKASKVIPVMLMGKL
. ****.* *.* .....*****.....*****. *****.*
CE AKDWTQKPPHPVPLYVHSYTSFSNTISSWCQYEALKYVSFPTQTICKASKVVVTMLMGRL
15 HP VSRRSYEHWEYLTATLISIGVSMFLLSSGPEPRSSPAT--TLSGLLLAGYIAFDSFTSN
*. ....** . *****.....* . * .....*.....* .....*
CE VRGQRYSWFEYCGCTIAFGASLFLSSSSKAGSSTITYTSFSGMILMAGYLLFDAFTLN
HP WQDALFAYK--MSSVQMMFGVNFFSCLFTVGSILLEQGALLEGTRFMGRHSEFAAHALLS
**.....* . *. ***** . . . **.....* .....* . * ..*.....
20 CE WQKALFDTKPKVSKYQMMFGVNFFSAILCAVSLIEQGLTWSSIKFGAEHVDFS RDVFLS
HP ICSACQLFIFYTIGQFGAAVFTIIMTLRQAFAILLSCLLYGHTVTVVGG LGVAVVFAAL
...* **...* .....* .....* .....* .....*
CE LSGAIGQIFIYSTIERFGPIVFAVIMTIRQIFIRNTLIRAEDHRGVEMAPPPPPPEPFRLK
HP LLRVYARGRLKQRGKKAVPVESPQVK
25 CE FLSMIIAVIHI

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Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. Z46196) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the

present invention.

<HP10671> (SEQ ID NOS: 127, 137, and 147)

Determination of the whole base sequence of the cDNA
5 insert of clone HP10671 obtained from cDNA library of human
thymus revealed the structure consisting of a 74-bp 5'-
untranslated region, a 921-bp ORF, and a 232-bp 3'-
untranslated region. The ORF encodes a protein consisting of
306 amino acid residues and there existed a putative
10 secretory signal at the N-terminus and one putative
transmembrane domain at the intermediate region. Figure 47
depicts the hydrophobicity/hydrophilicity profile, obtained
by the Kyte-Doolittle method, of the present protein.

Furthermore, the search of the GenBank using the base
15 sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. AA357141) among ESTs. However, since
they are partial sequences, it can not be judged whether or
not they encode the same protein as the protein of the
20 present invention.

<HP10673> (SEQ ID NOS: 128, 138, and 148)

Determination of the whole base sequence of the cDNA
insert of clone HP10673 obtained from cDNA library of the
25 human thymus revealed the structure consisting of a 203-bp
5'-untranslated region, a 1668-bp ORF, and a 339-bp 3'-
untranslated region. The ORF encodes a protein consisting of
555 amino acid residues and there existed one putative
transmembrane domain. Figure 48 depicts the
30 hydrophobicity/hydrophilicity profile, obtained by the Kyte-
Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product

of 65 kDa that was somewhat larger than the molecular weight of 61,781 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R96413) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10675> (SEQ ID NOS: 129, 139, and 149)

Determination of the whole base sequence of the cDNA insert of clone HP10675 obtained from cDNA library of the human thymus revealed the structure consisting of a 92-bp 5'-untranslated region, a 753-bp ORF, and a 648-bp 3'-untranslated region. The ORF encodes a protein consisting of 250 amino acid residues and there existed at least one putative transmembrane domain. Figure 49 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA356139) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10683> (SEQ ID NOS: 130, 140, and 150)

Determination of the whole base sequence of the cDNA insert of clone HP10683 obtained from cDNA library of the human lymphoma cell line U937 revealed the structure

consisting of a 25-bp 5'-untranslated region, a 525-bp ORF, and a 714-bp 3'-untranslated region. The ORF encodes a protein consisting of 174 amino acid residues and there existed one putative transmembrane domain. Figure 50 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 22 kDa that was somewhat larger than the molecular weight of 19,572 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 24 kDa to which sugar chains are presumably attached. In addition, there exist in the amino acid sequence of this protein one site at which N-glycosylation may occur (Asn-Ile-Thr at position 27).

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA482321) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

INDUSTRIAL APPLICABILITY

The present invention provides human proteins having hydrophobic domains, DNAs encoding these proteins, and expression vectors for these DNAs as well as eukaryotic cells expressing these DNAs. Since all of the proteins of the present invention are secreted or exist in the cell membrane, they are considered to be proteins controlling the proliferation and/or the differentiation of the cells. Accordingly, the proteins of the present invention can be employed as pharmaceuticals such as carcinostatic agents

which act to control the proliferation and/or the differentiation of the cells, or as antigens for preparing antibodies against these proteins. The DNAs of the present invention can be utilized as probes for the genetic diagnosis and gene sources for the gene therapy. Furthermore, the DNAs can be utilized for large-scale expression of these proteins. Cells into which these genes are introduced to express these proteins, can be utilized for detection of the corresponding receptors or ligands, screening of novel small molecule pharmaceuticals and the like.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The

desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, Trends Pharmacol. Sci. 15(7): 250-254; 5 Lavarosky et al., 1997, Biochem. Mol. Med. 62(1): 11-22; and Hampel, 1998, Prog. Nucleic Acid Res. Mol. Biol. 58: 1-39; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed 10 herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or 15 that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been 20 partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, 25 of transposable elements (Plasterk, 1992, Bioessays 14(9): 629-633; Zwaal et al., 1993, Proc. Natl. Acad. Sci. USA 90(16): 7431-7435; Clark et al., 1994, Proc. Natl. Acad. Sci. USA 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, 30 preferably detected by positive/negative genetic selection strategies (Mansour et al., 1988, Nature 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153;

5,614, 396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s). Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that share at least 75%

sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. As used
5 herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide, as
10 determined by those of skill in the art. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the
15 disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous, or related to that encoded by the polynucleotides.

The invention also includes polynucleotides with
20 sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing under reduced stringency conditions, more preferably stringent conditions, and most preferably
25 highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the Table 32 below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for
30 example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 32

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) [†]	Hybridization Temperature and Buffer [†]	Wash Temperature and Buffer [†]
A	DNA : DNA	≥50	65°C; 1×SSC -or- 42°C; 1×SSC, 50% formamide	65°C; 0.3×SSC
B	DNA : DNA	<50	T _B *; 1×SSC	T _B *; 1×SSC
C	DNA : RNA	≥50	67°C; 1×SSC -or- 45°C; 1×SSC, 50% formamide	67°C; 0.3×SSC
D	DNA : RNA	<50	T _D *; 1×SSC	T _D *; 1×SSC
E	RNA : RNA	≥50	70°C; 1×SSC -or- 50°C; 1×SSC, 50% formamide	70°C; 0.3×SSC
F	RNA : RNA	<50	T _F *; 1×SSC	T _F *; 1×SSC
G	DNA : DNA	≥50	65°C; 4×SSC -or- 42°C; 4×SSC, 50% formamide	65°C; 1×SSC
H	DNA : DNA	<50	T _H *; 4×SSC	T _H *; 4×SSC
I	DNA : RNA	≥50	67°C; 4×SSC -or- 45°C; 4×SSC, 50% formamide	67°C; 1×SSC
J	DNA : RNA	<50	T _J *; 4×SSC	T _J *; 4×SSC
K	RNA : RNA	≥50	70°C; 4×SSC -or- 50°C; 4×SSC, 50% formamide	67°C; 1×SSC
L	RNA : RNA	<50	T _L *; 2×SSC	T _L *; 2×SSC
M	DNA : DNA	≥50	50°C; 4×SSC -or- 40°C; 6×SSC, 50% formamide	50°C; 2×SSC
N	DNA : DNA	<50	T _N *; 6×SSC	T _N *; 6×SSC
O	DNA : RNA	≥50	55°C; 4×SSC -or- 42°C; 6×SSC, 50% formamide	55°C; 2×SSC
P	DNA : RNA	<50	T _P *; 6×SSC	T _P *; 6×SSC
Q	RNA : RNA	≥50	60°C; 4×SSC -or- 45°C; 6×SSC, 50% formamide	60°C; 2×SSC
R	RNA : RNA	<50	T _R *; 4×SSC	T _R *; 4×SSC

‡ : The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

† : SSPE (1×SSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH7.4) can be substituted for SSC (1×SSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R : The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C)=2(#of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C)=81.5 + 16.6(log₁₀[Na⁺]) + 0.41 (%G+C) · (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1×SSC=0.165M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and Current Protocols in Molecular Biology, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing

polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

CLAIMS

1. A protein comprising any one of an amino acid sequence selected from the group consisting of SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130.
2. An isolated DNA encoding the protein according to Claim 1.
3. An isolated cDNA comprising any one of a base sequence selected from the group consisting of SEQ ID NOS: 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140.
4. The cDNA according to Claim 3 consisting of any one of a base sequence selected from the group consisting of SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120, and 141 to 150.
5. An expression vector that is capable of expressing the DNA according to any one of Claim 2 to Claim 4 by in vitro translation or in eukaryotic cells.
6. A transformed eukaryotic cell that is capable of expressing the DNA according to any one of Claim 2 to Claim 4 and of producing the protein according to Claim 1.

1/50

Fig.1

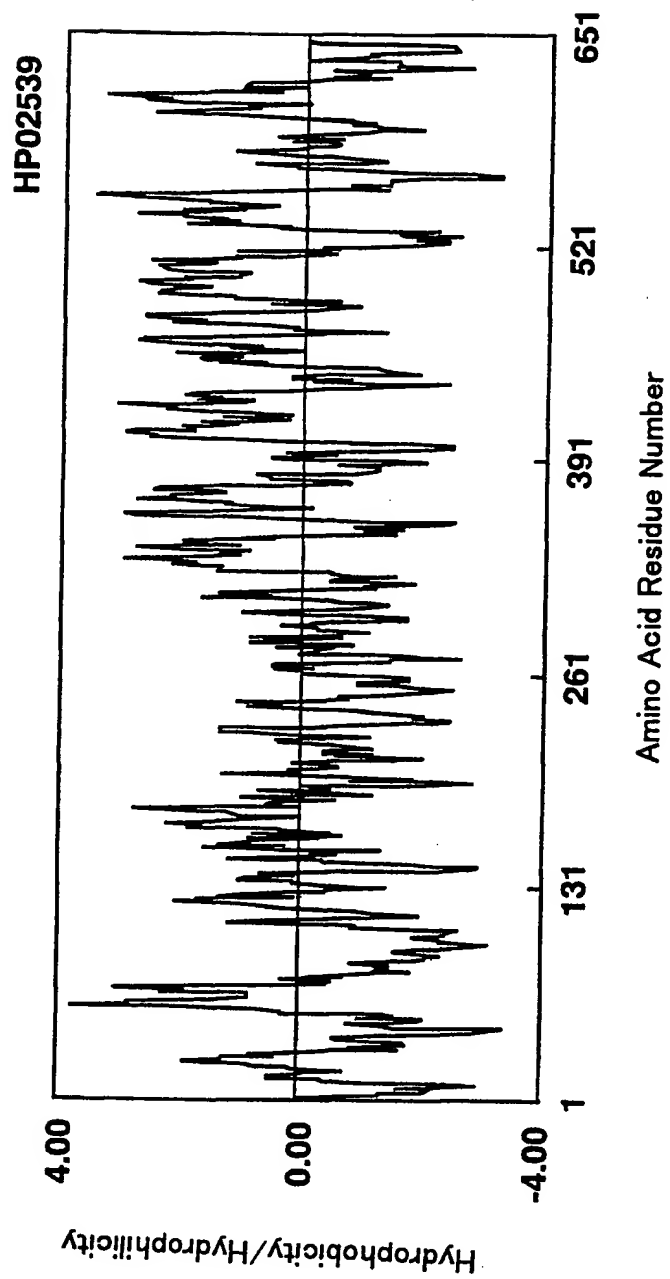
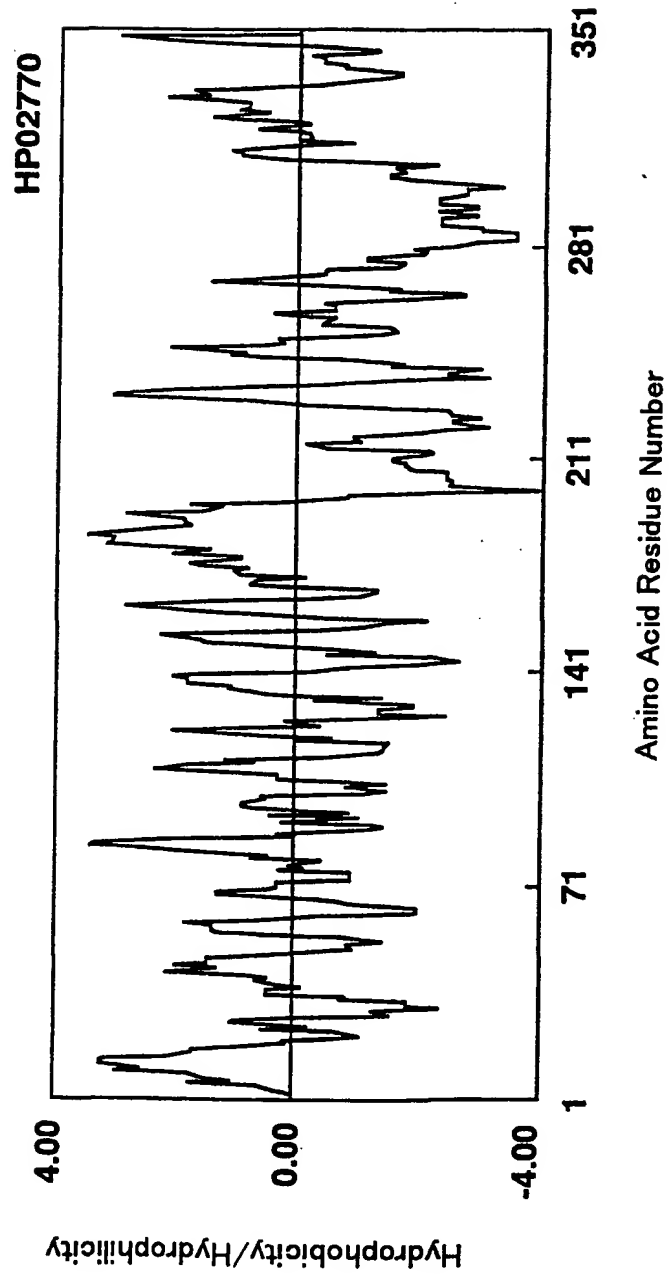
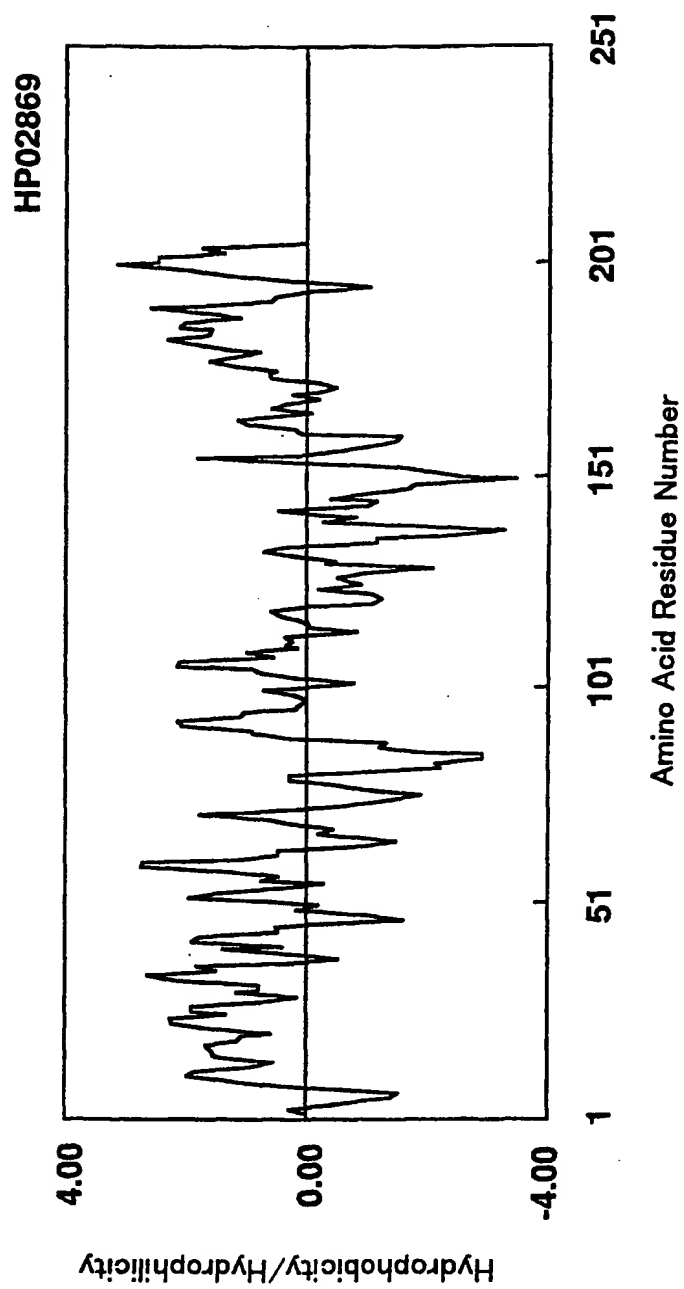


Fig.2



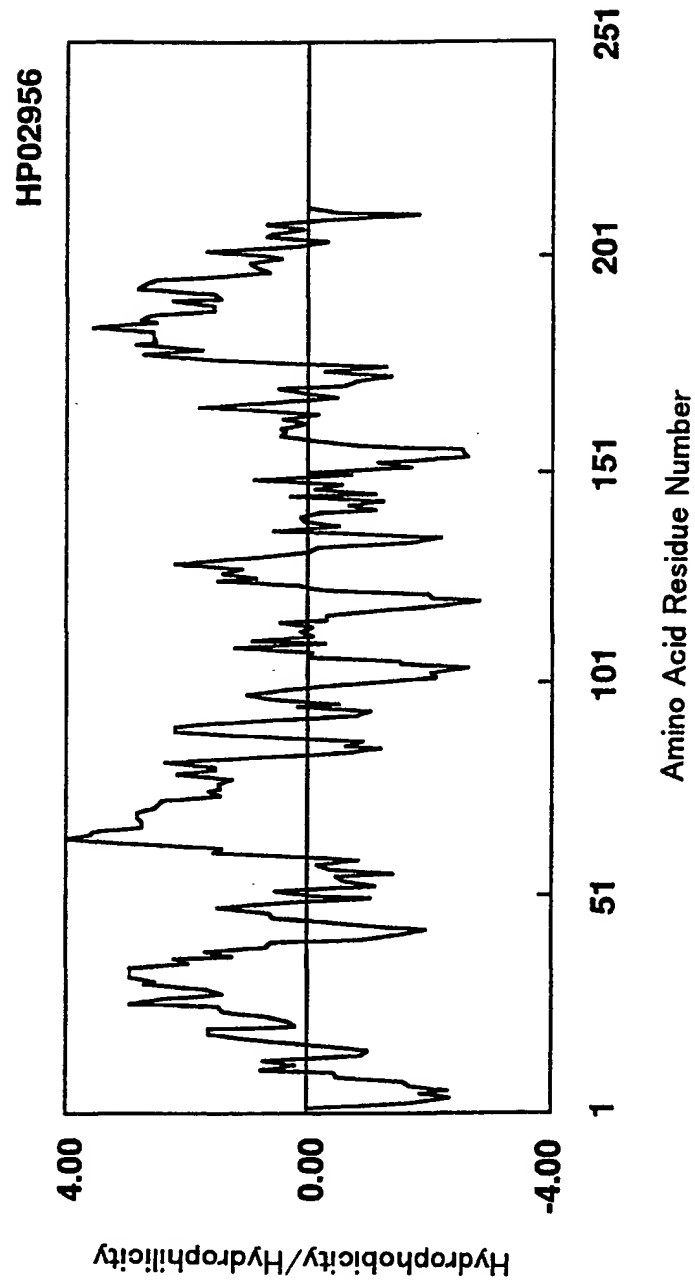
3/50

Fig.3



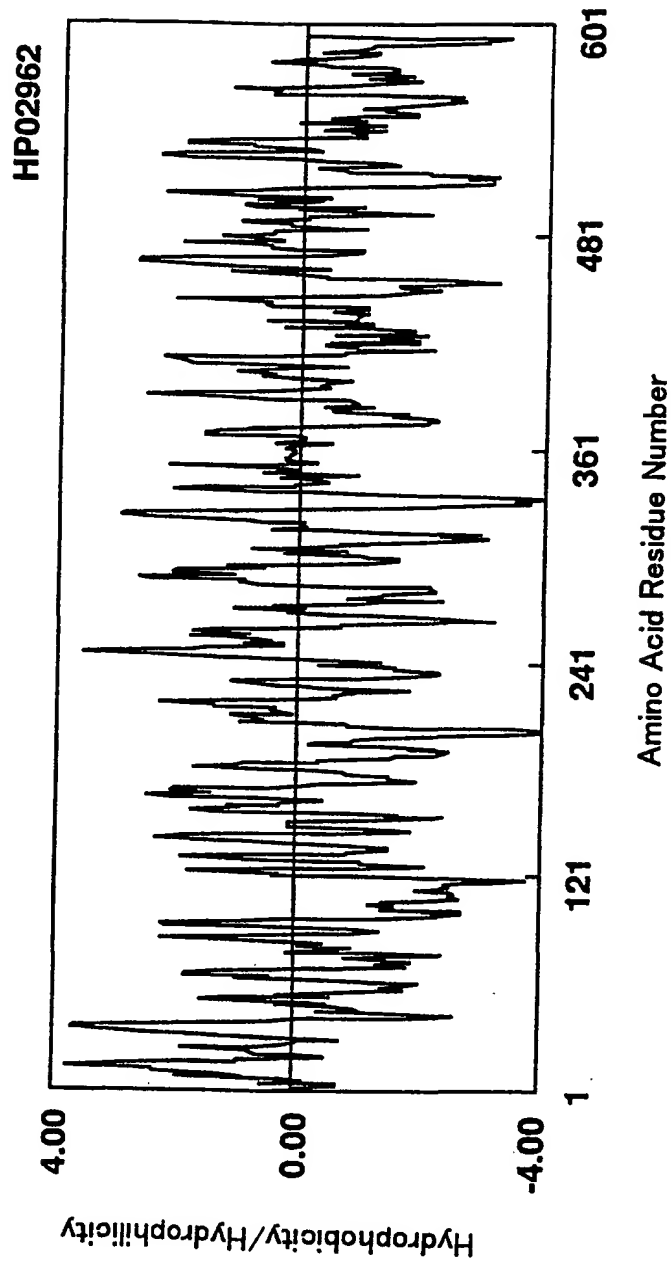
4/50

Fig.4



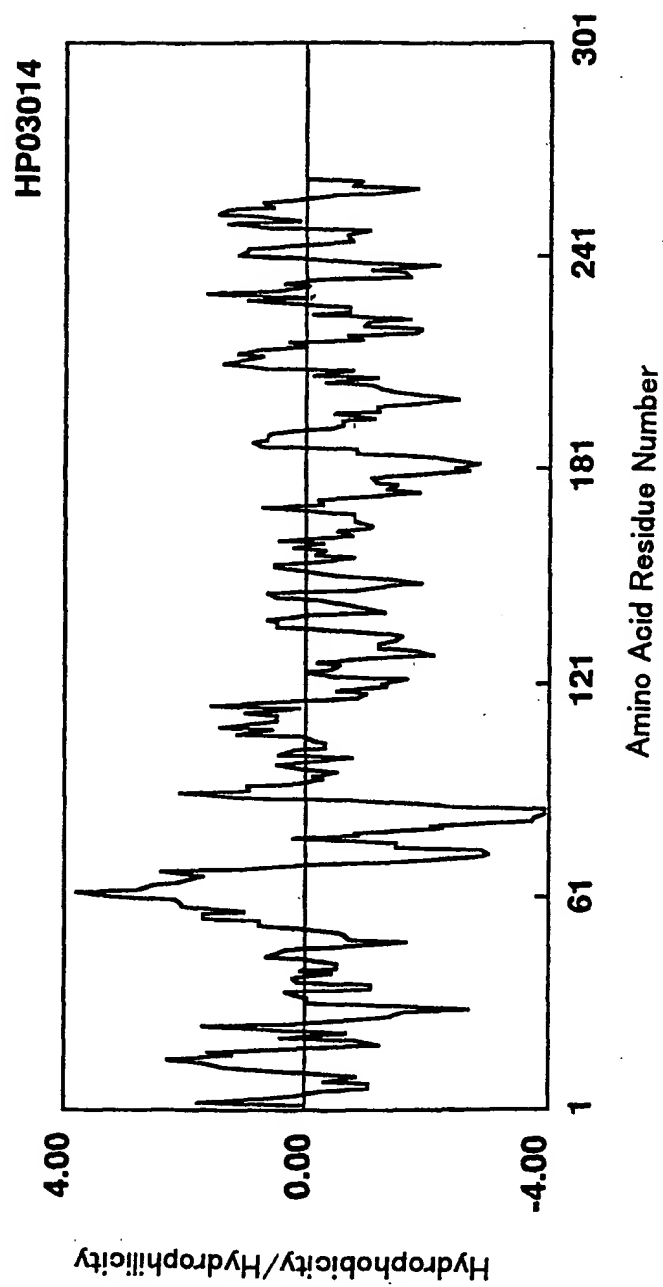
5/50

Fig.5



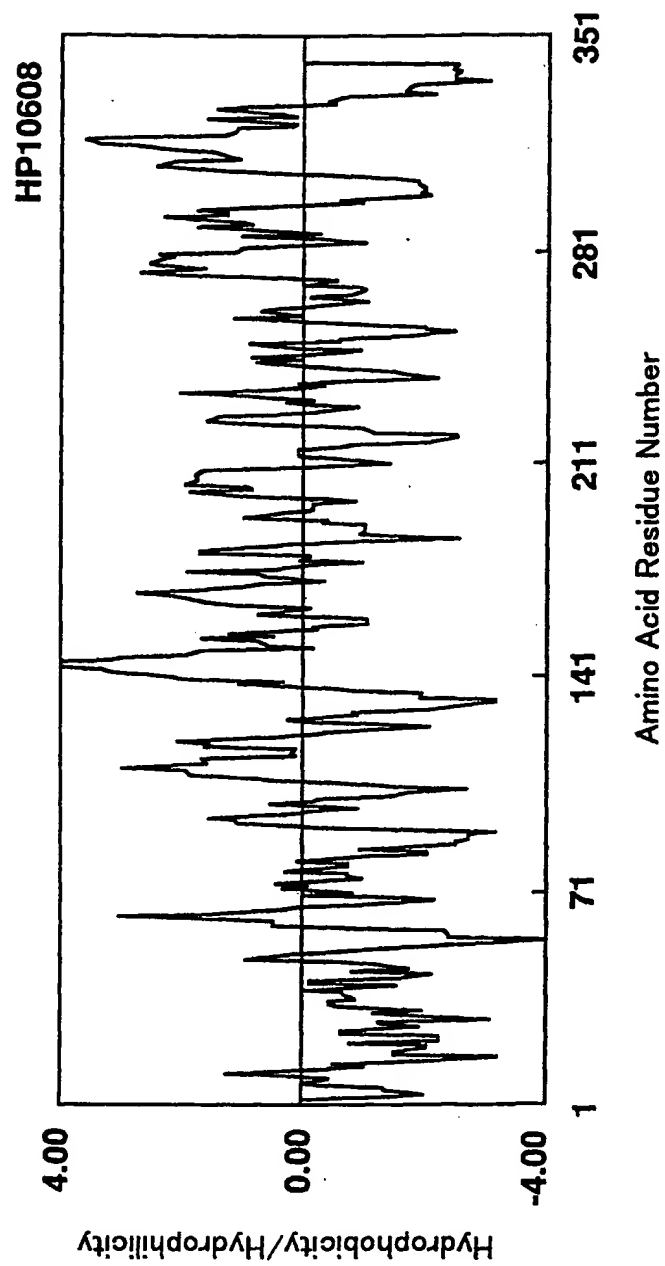
6/50

Fig.6



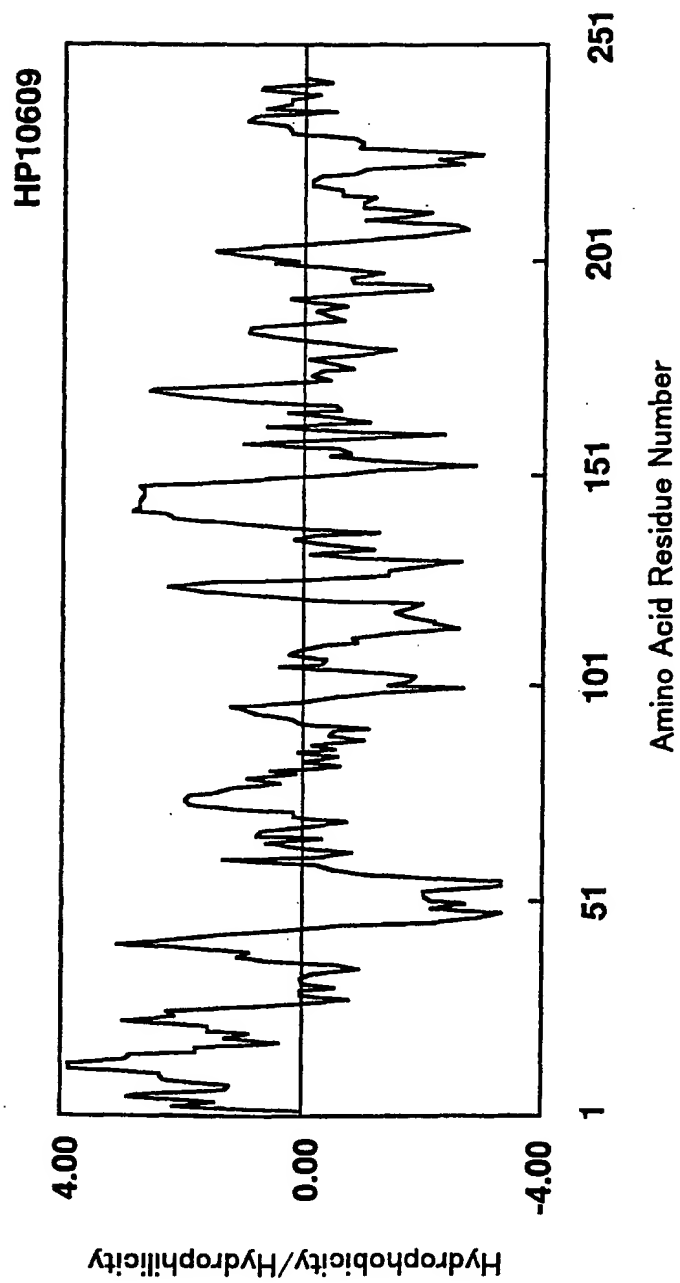
7/50

Fig.7



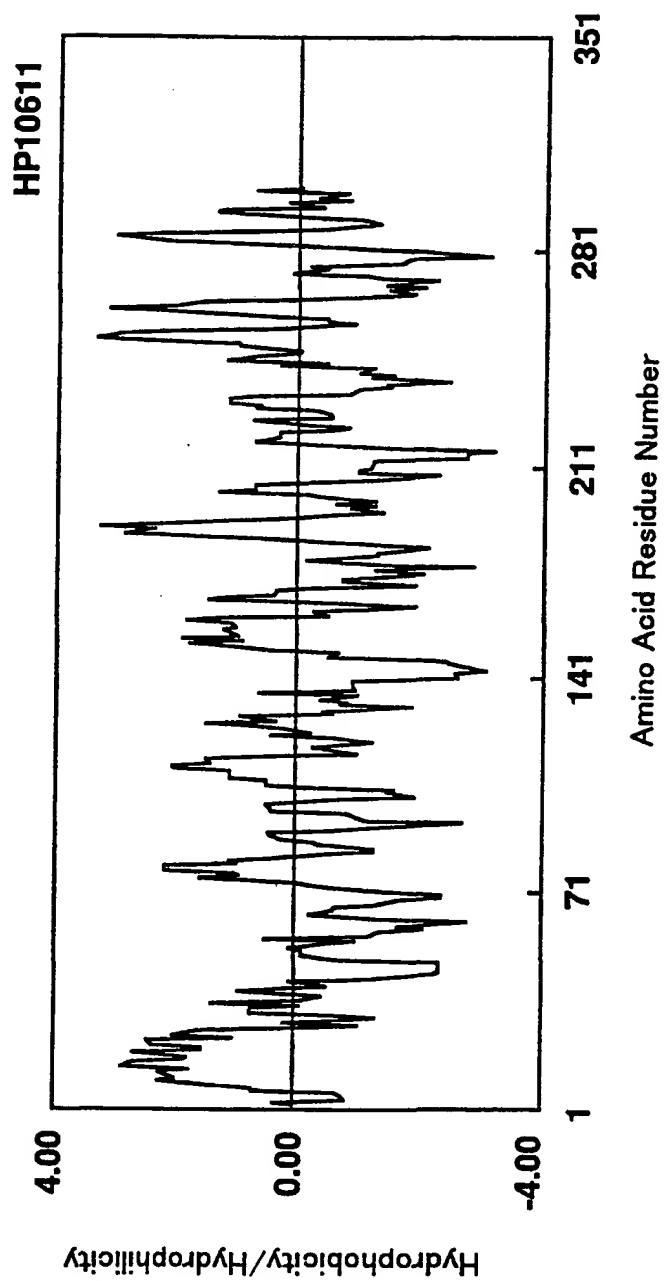
8/50

Fig.8



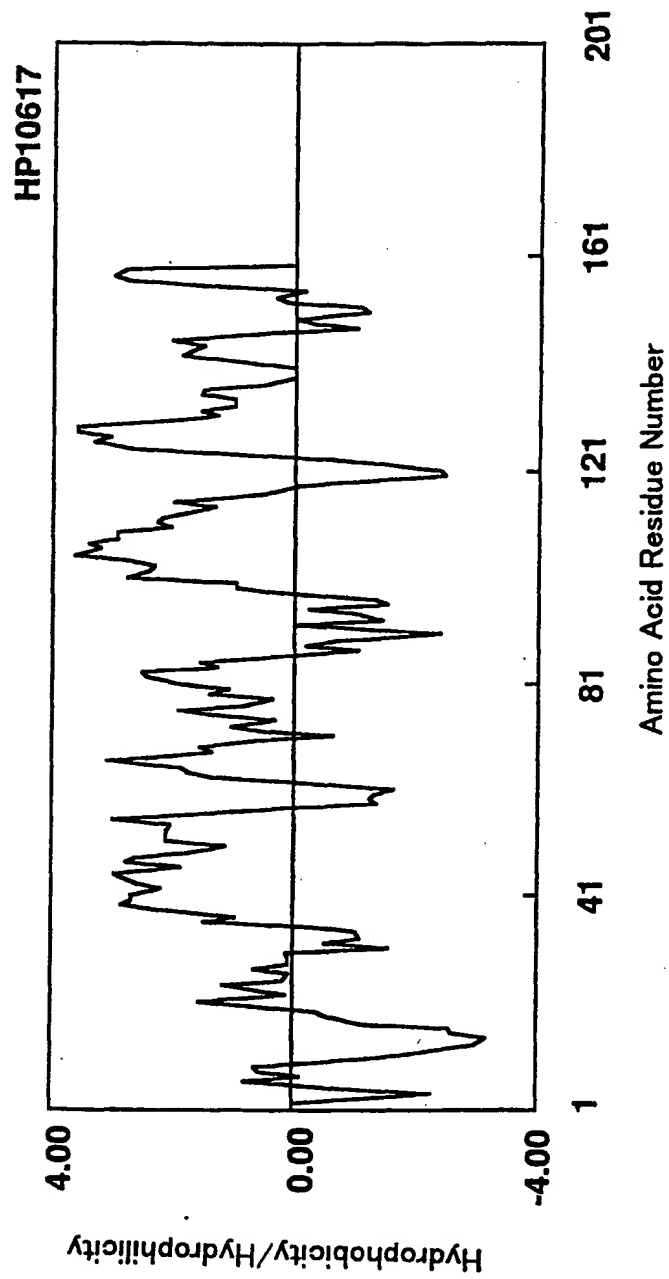
9/50

Fig. 9

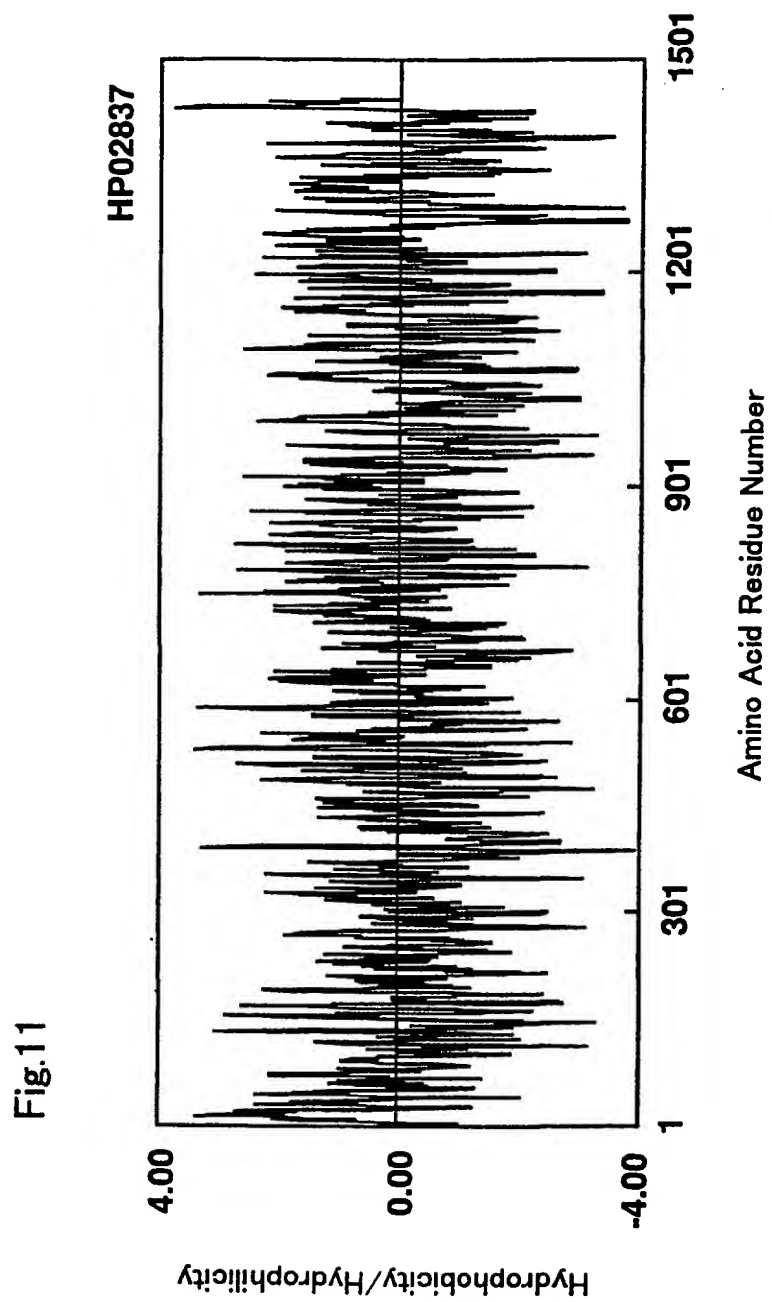


10/50

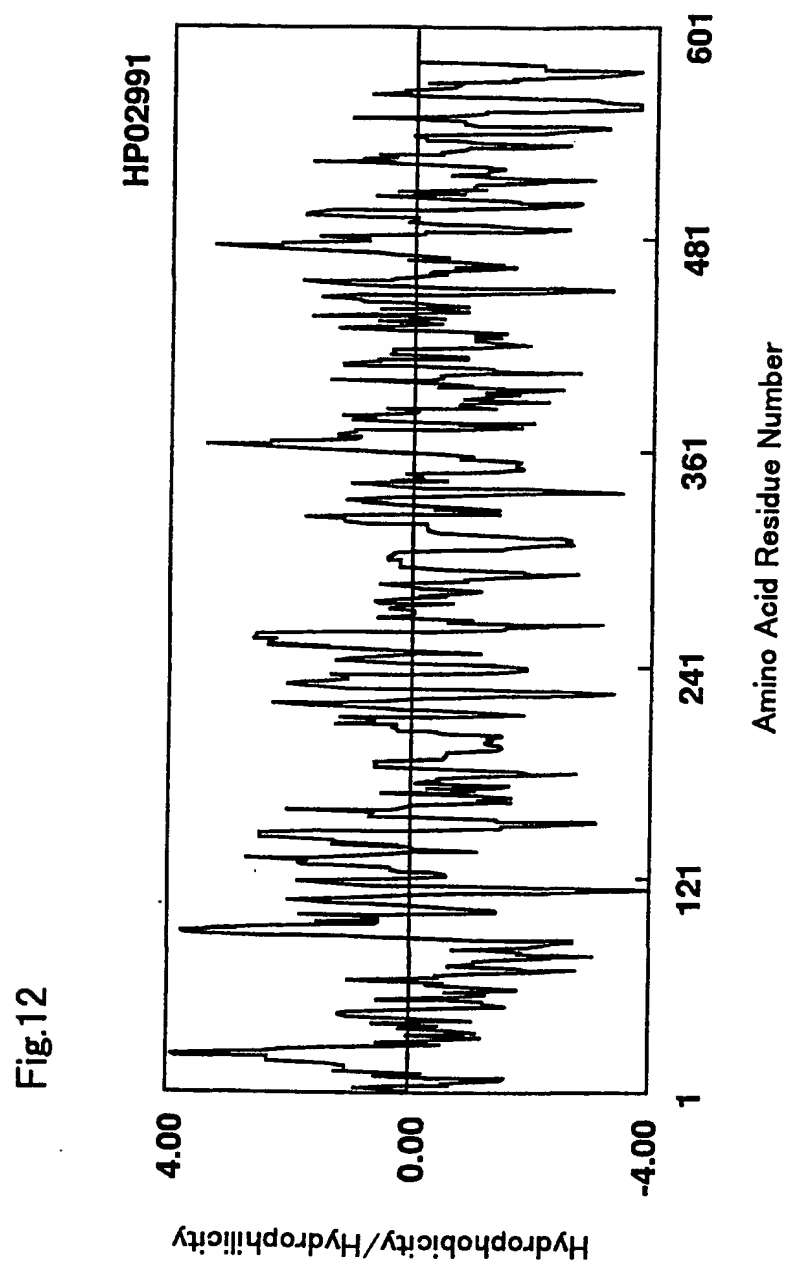
Fig.10



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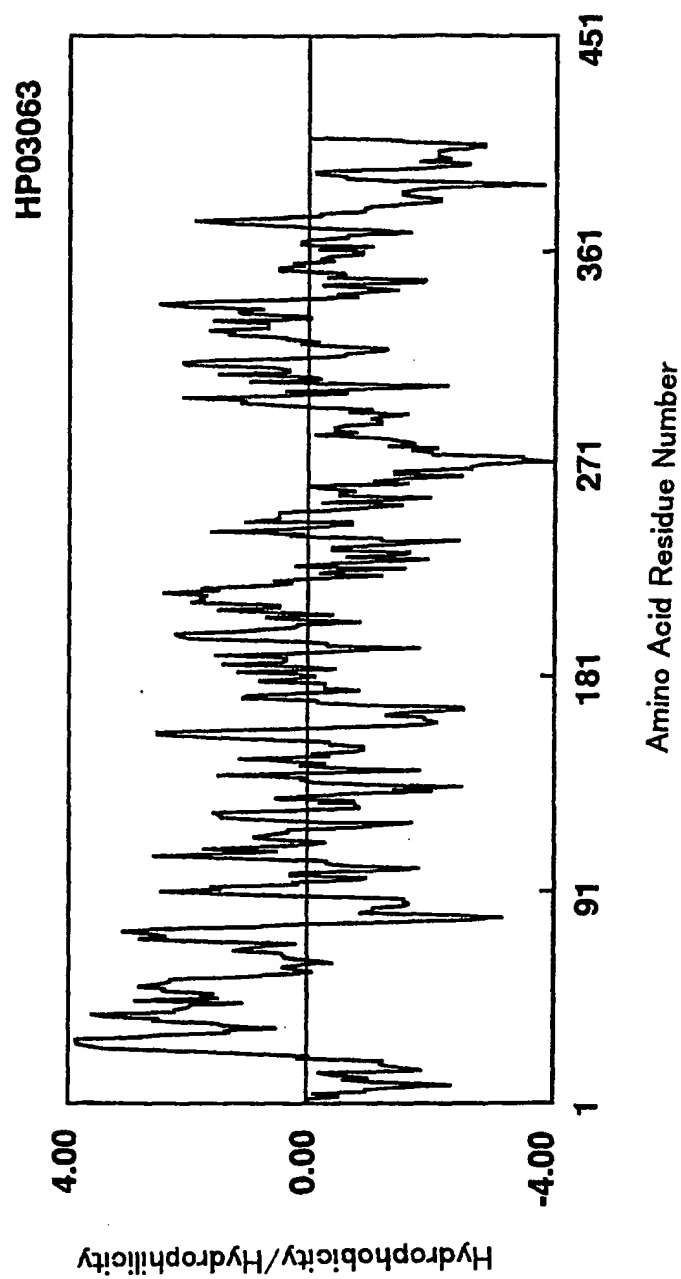


12/50



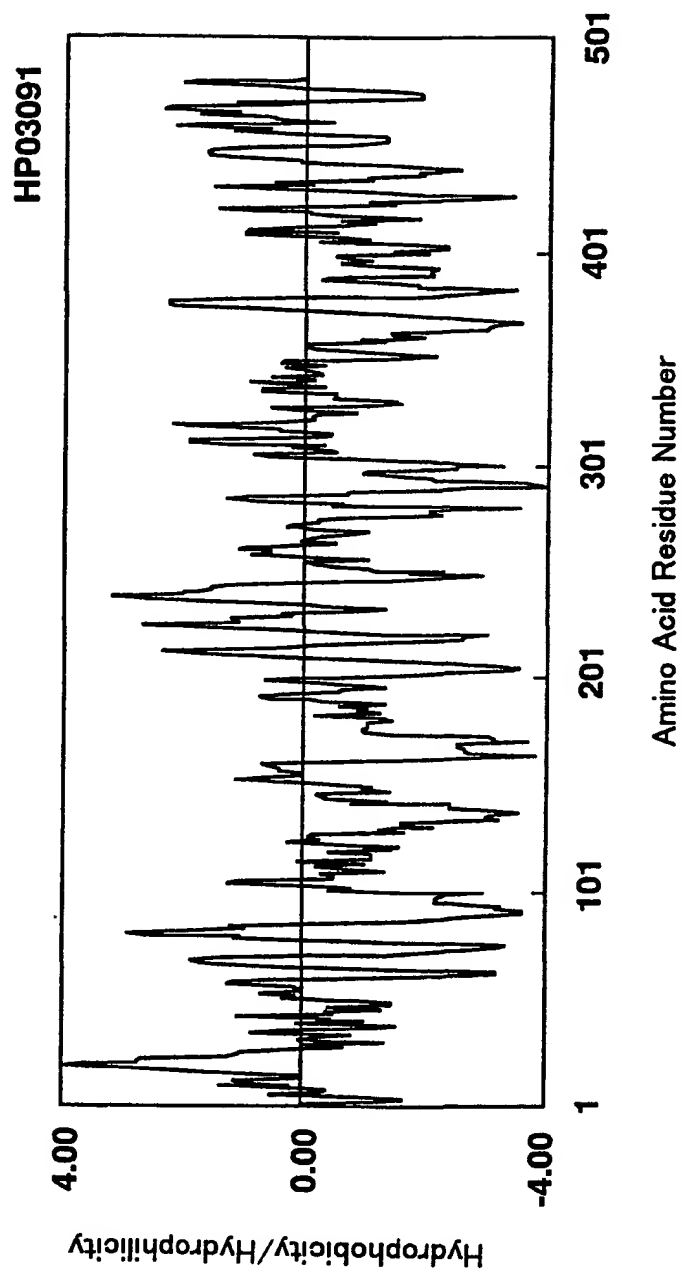
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Fig.13



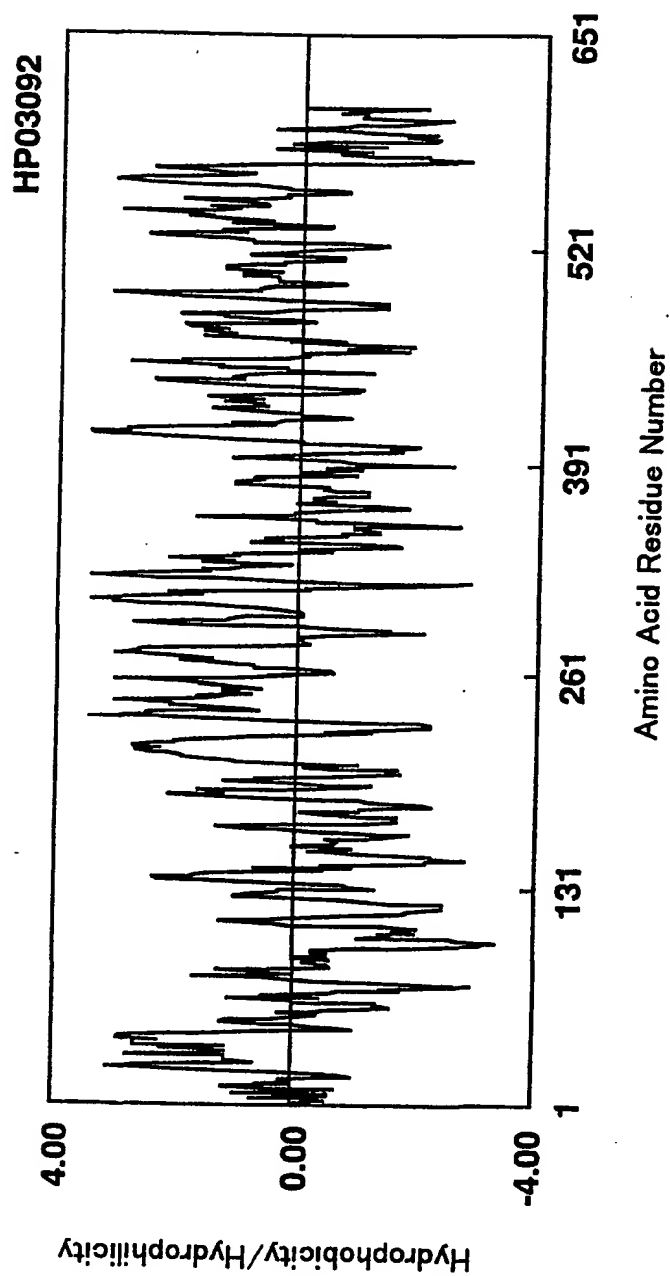
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Fig.14



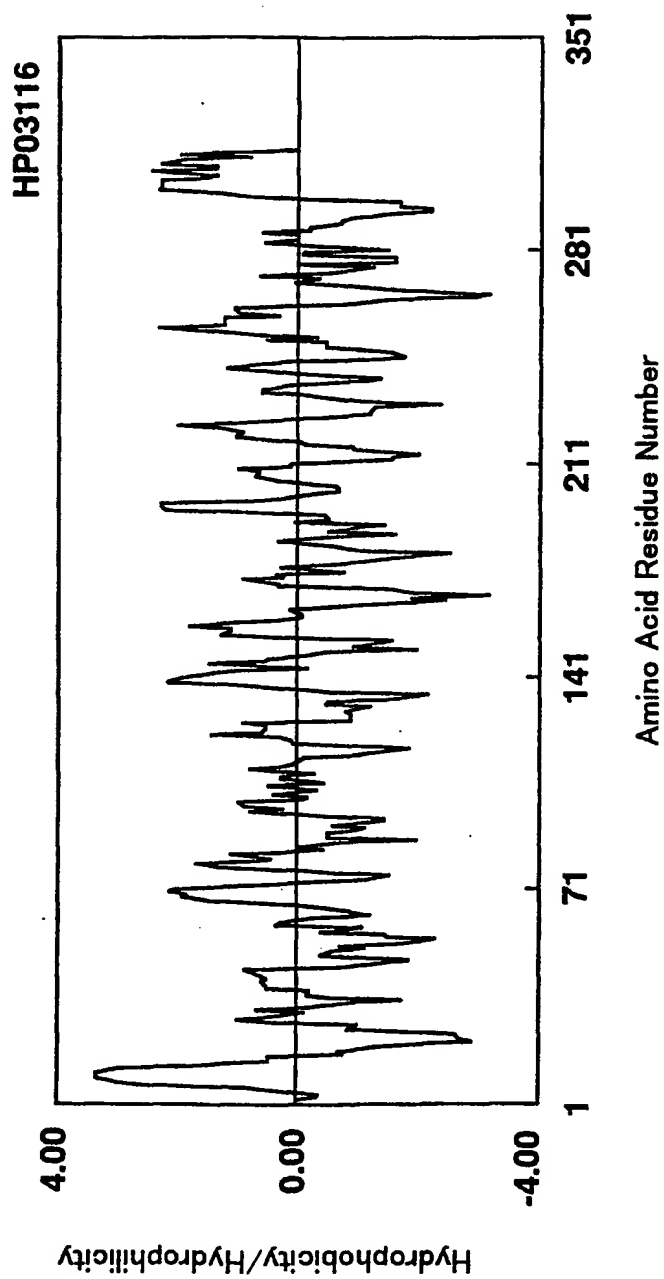
15/50

Fig.15



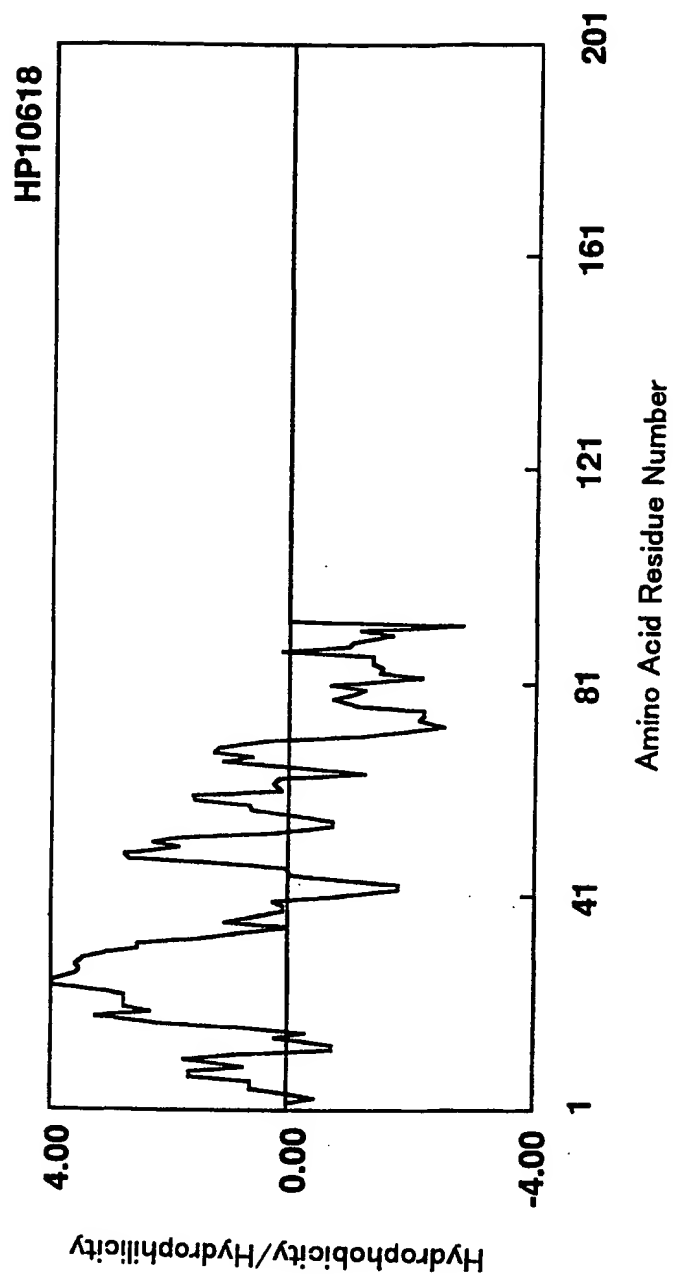
16/50

Fig.16



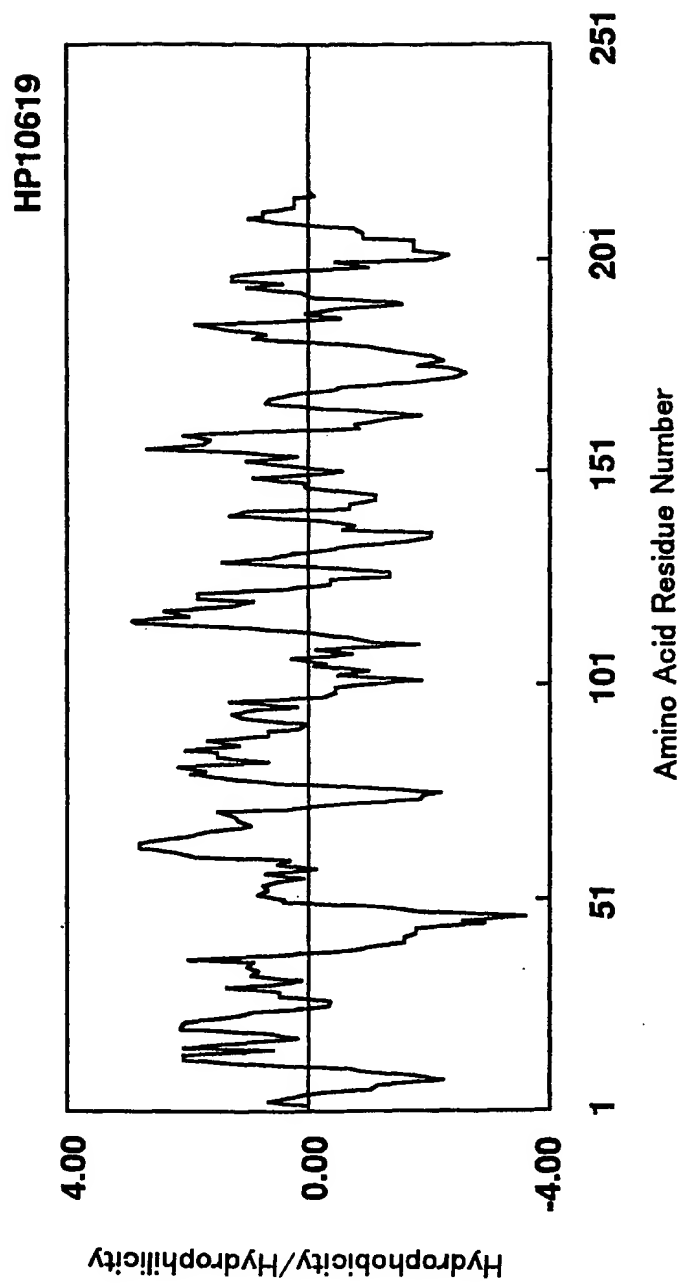
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Fig.17



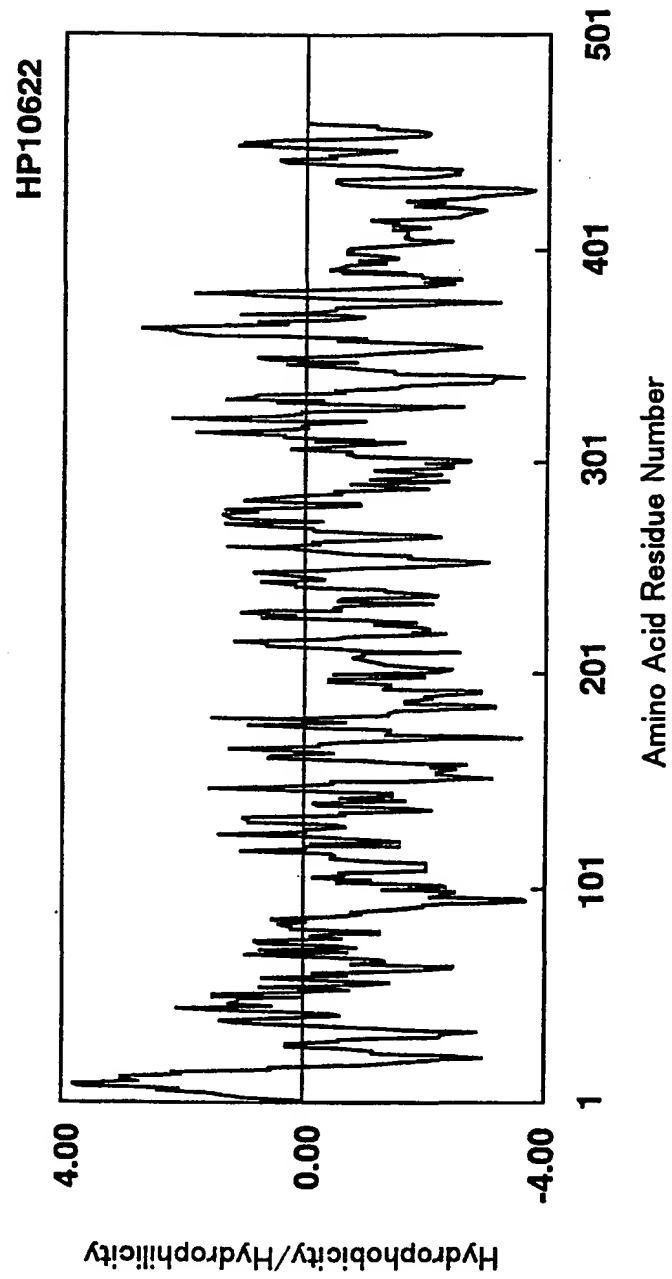
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Fig.18



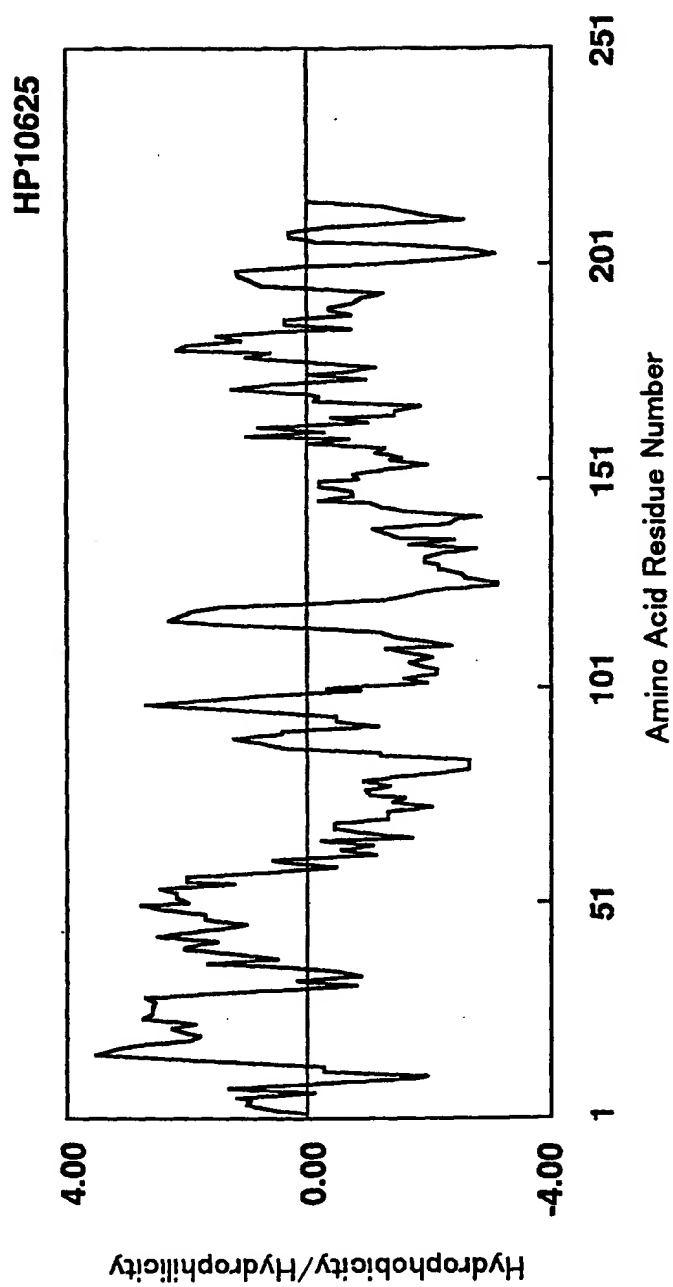
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Fig.19



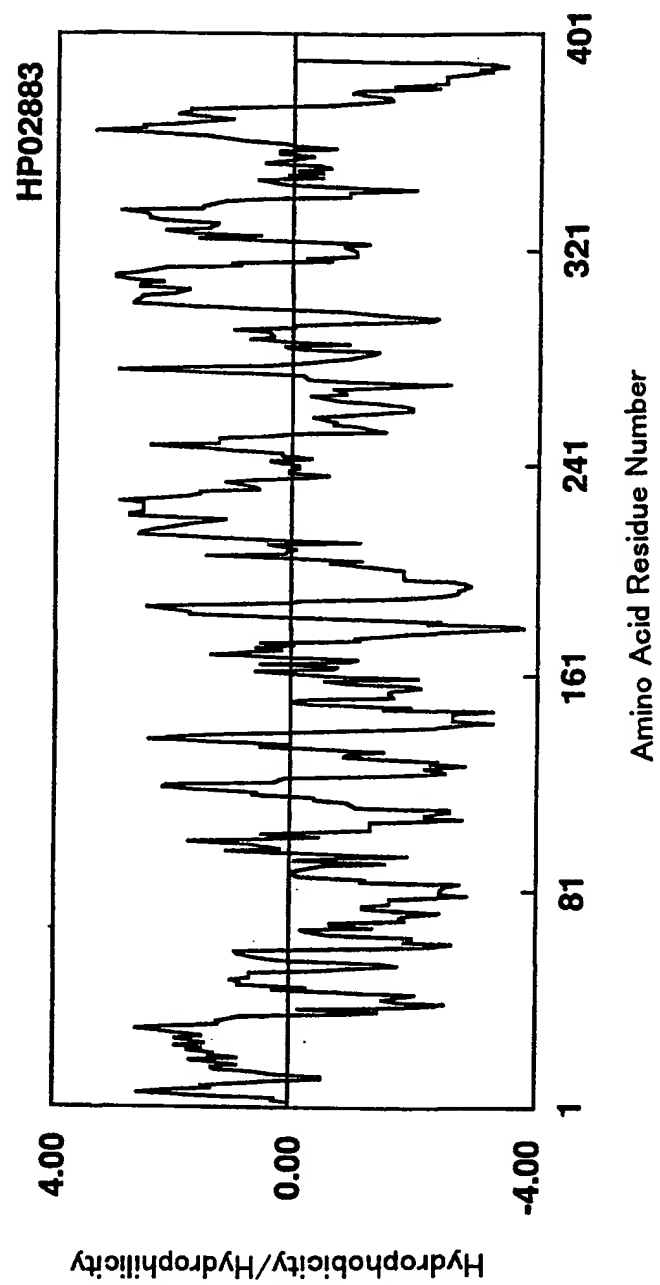
20/50

Fig.20



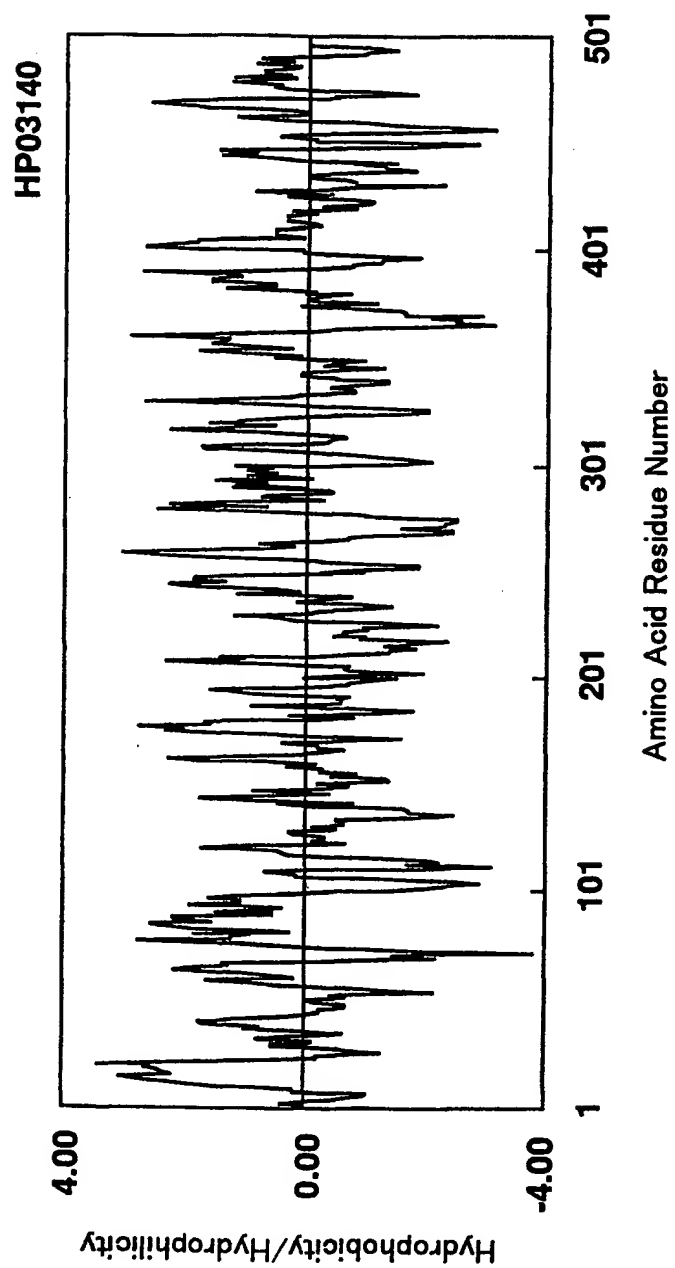
21/50

Fig.21



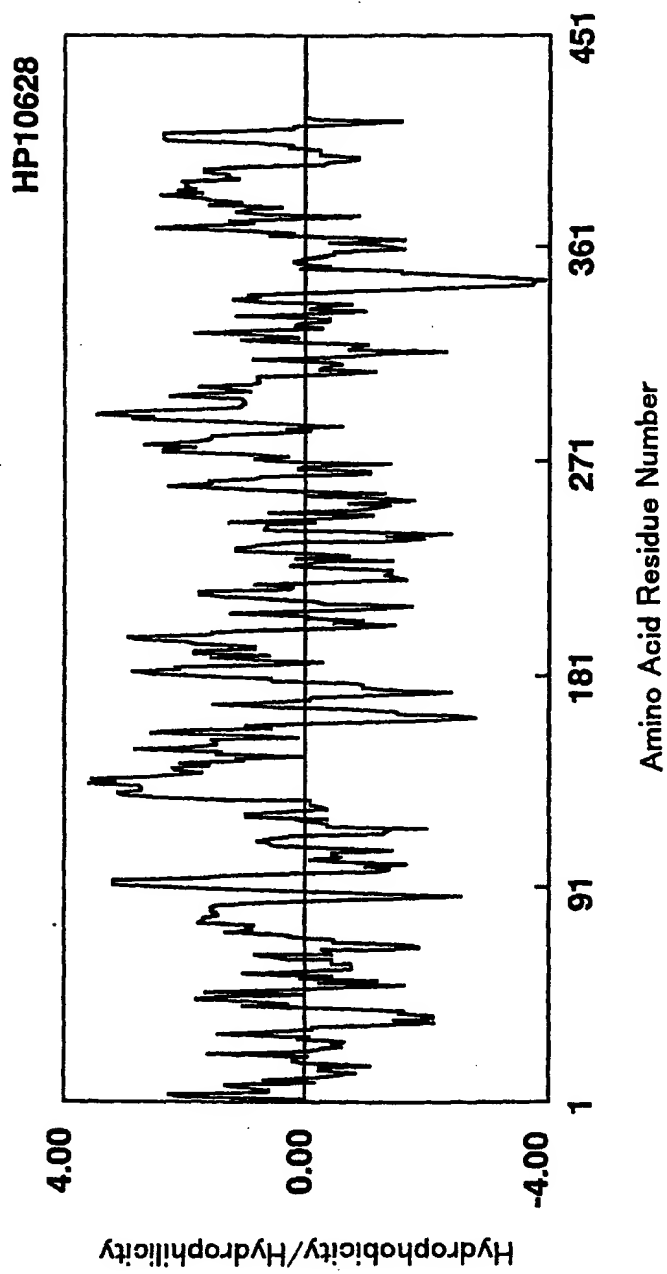
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Fig.22



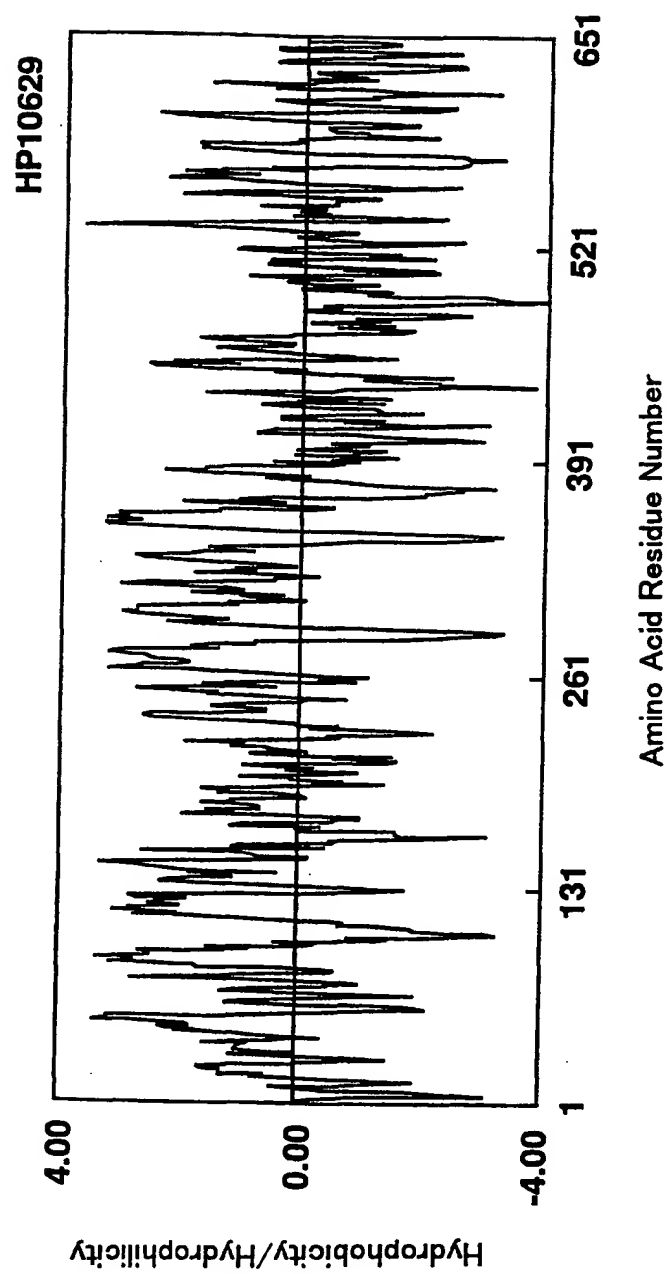
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Fig.23



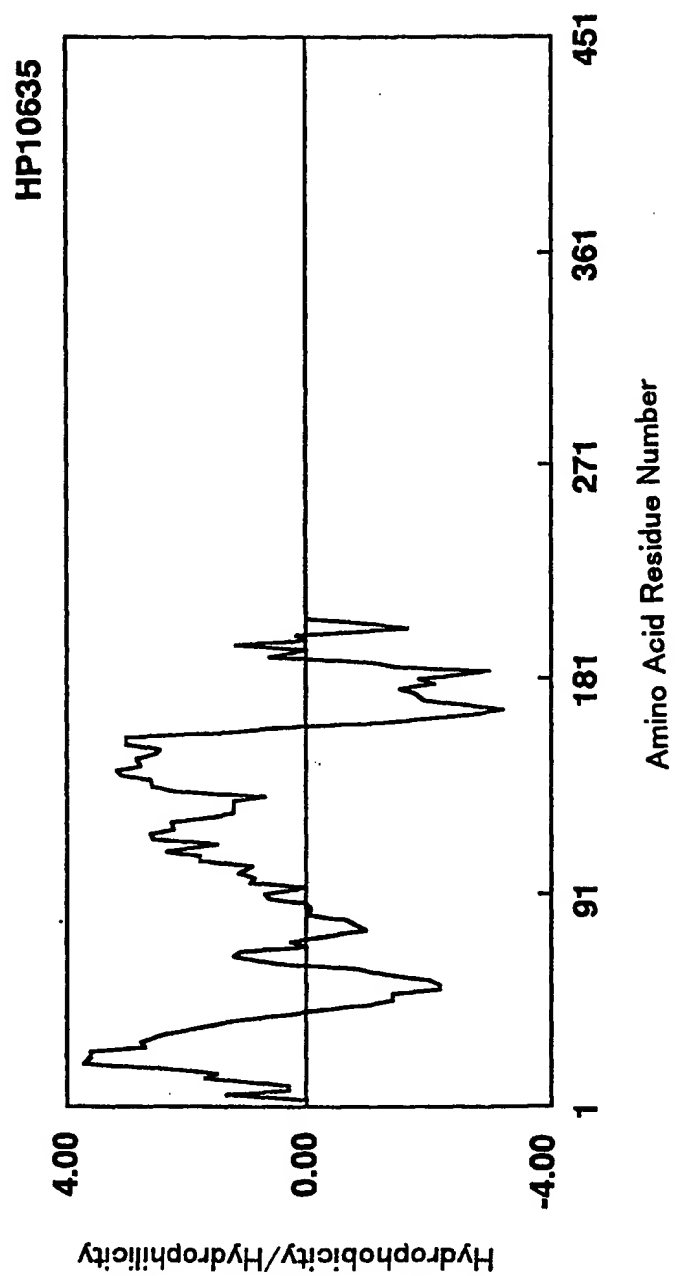
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Fig.24



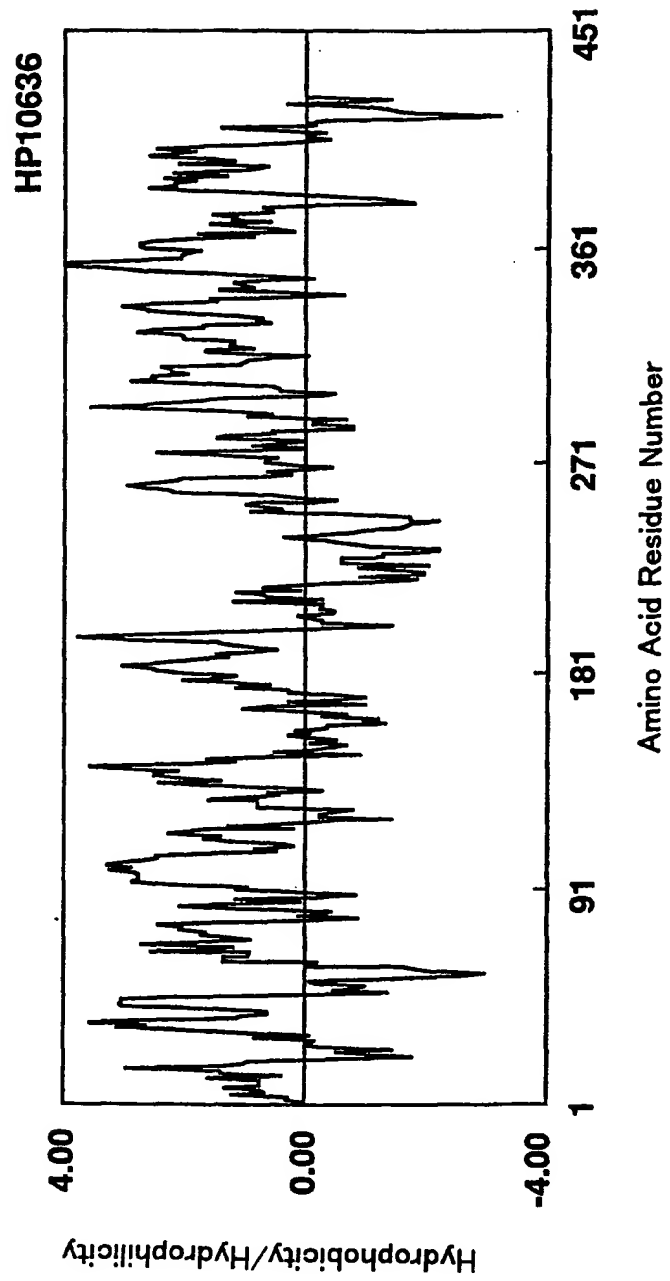
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Fig.25



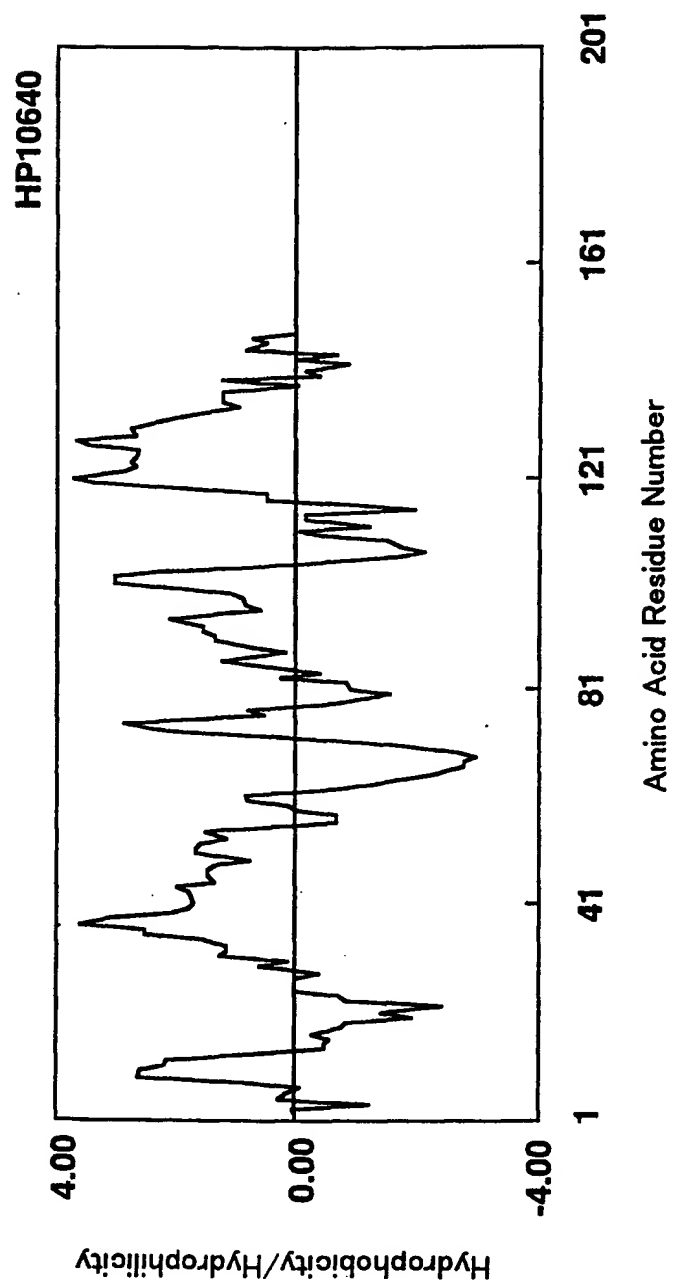
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Fig.26



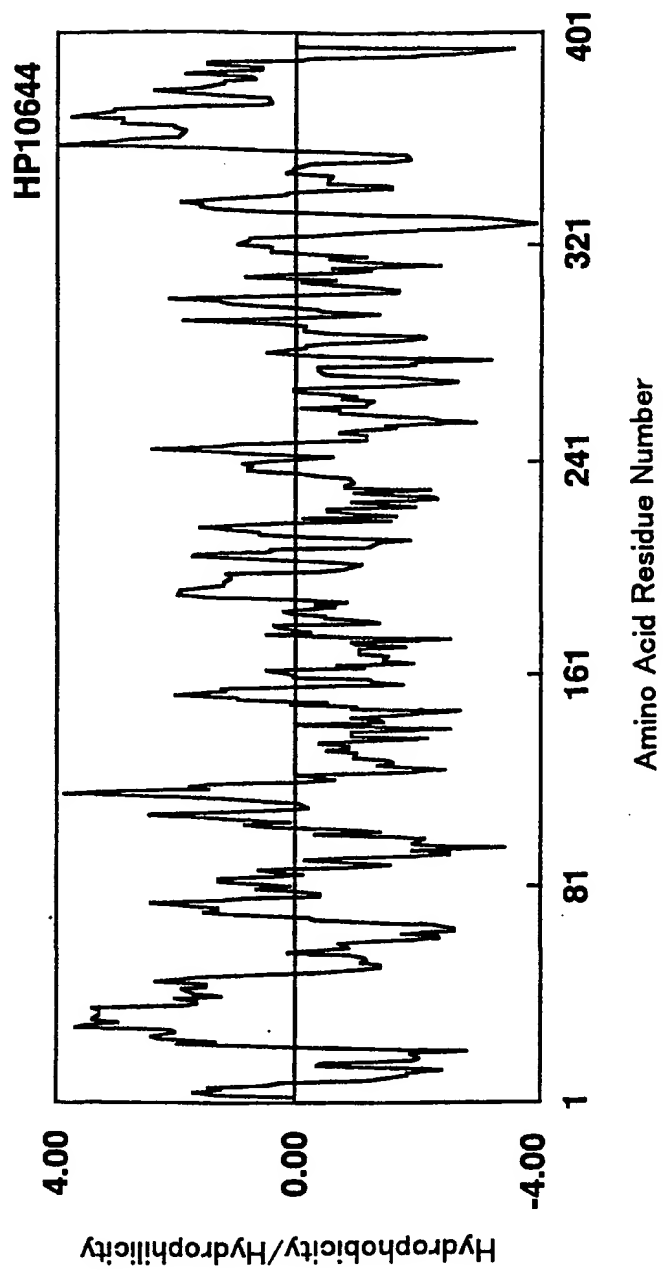
27/50

Fig.27



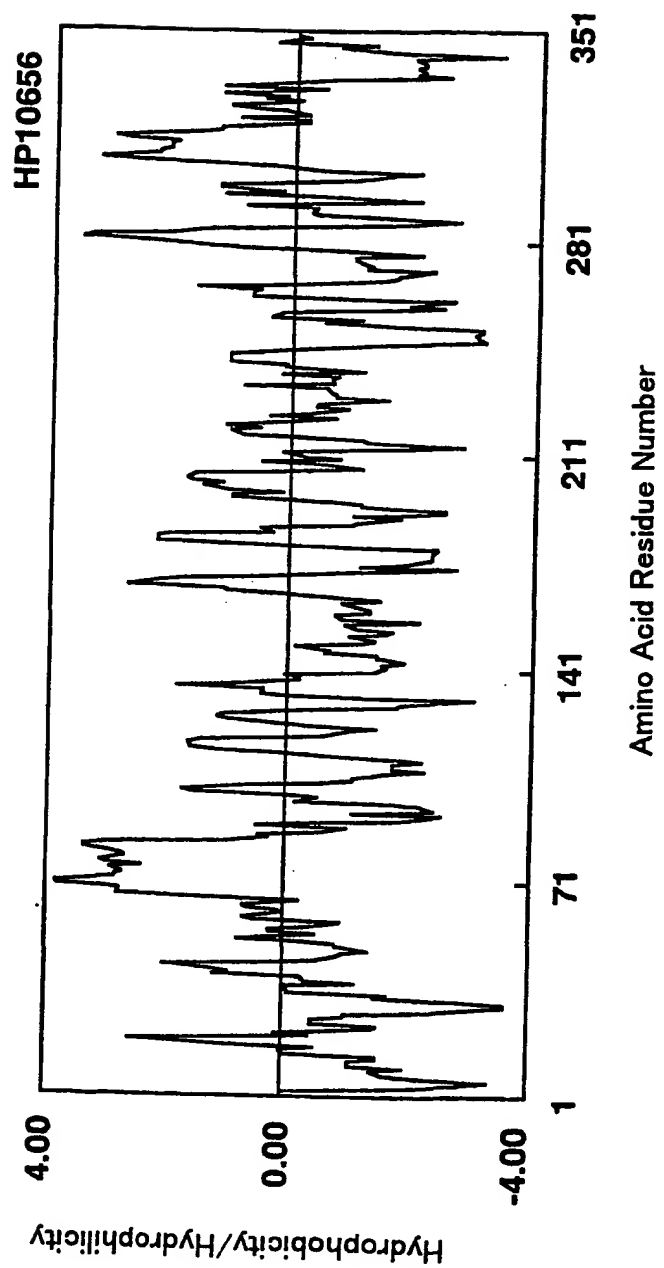
28/50

Fig.28



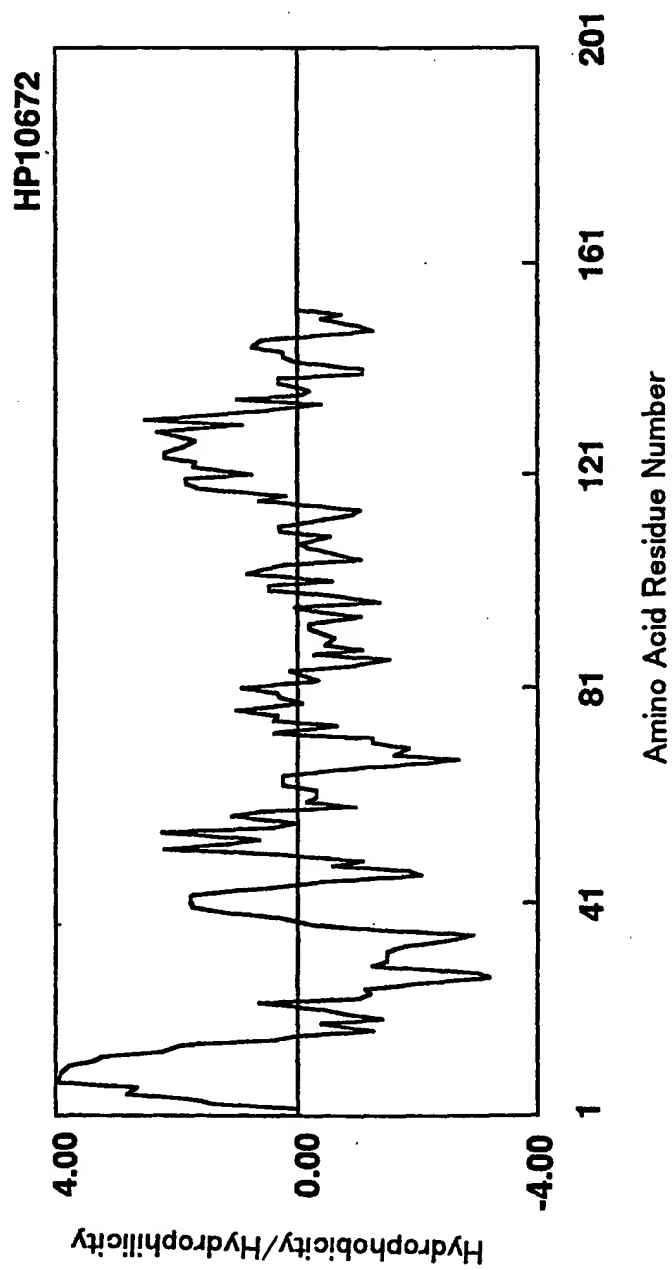
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Fig.29

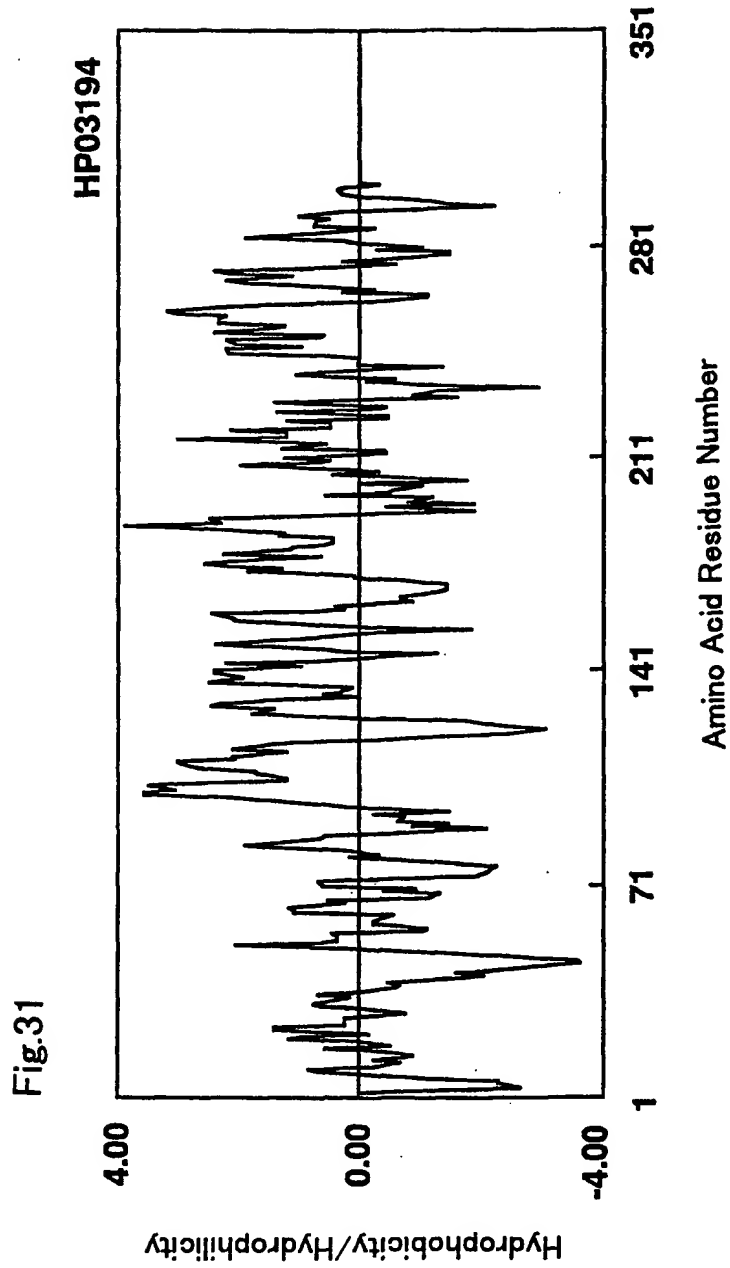


30/50

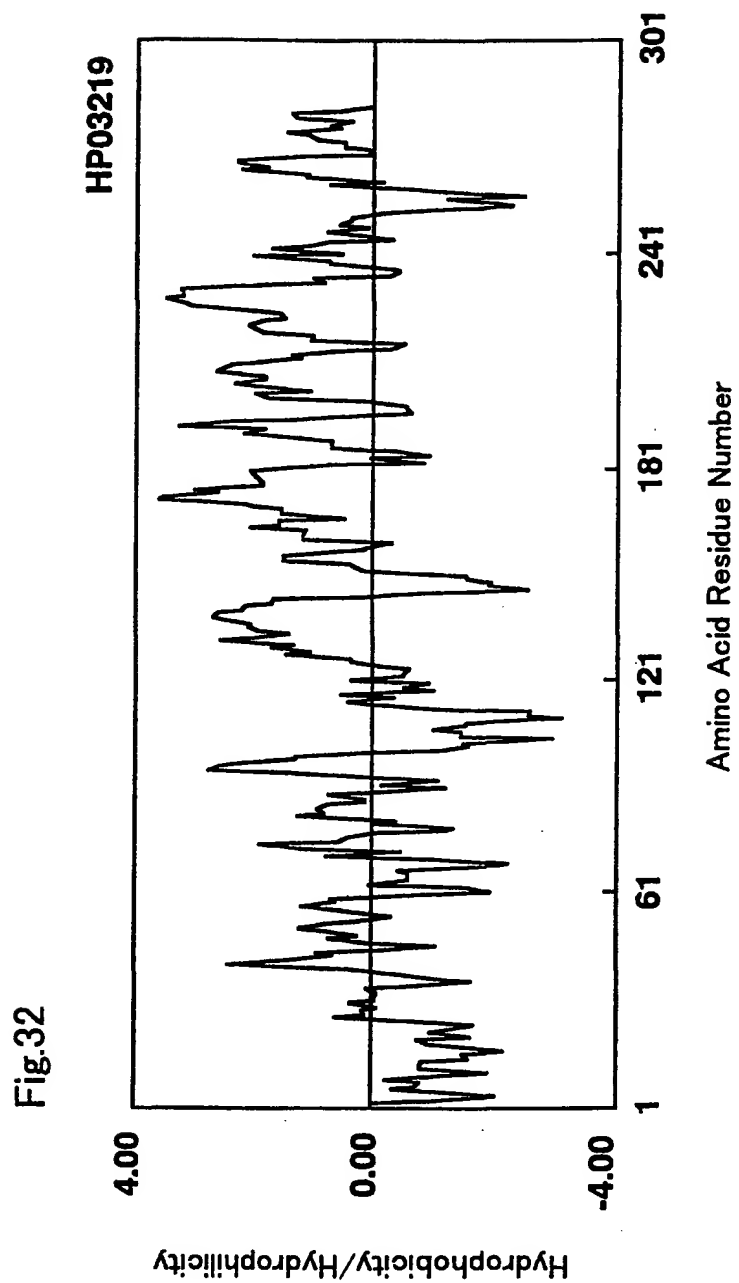
Fig.30



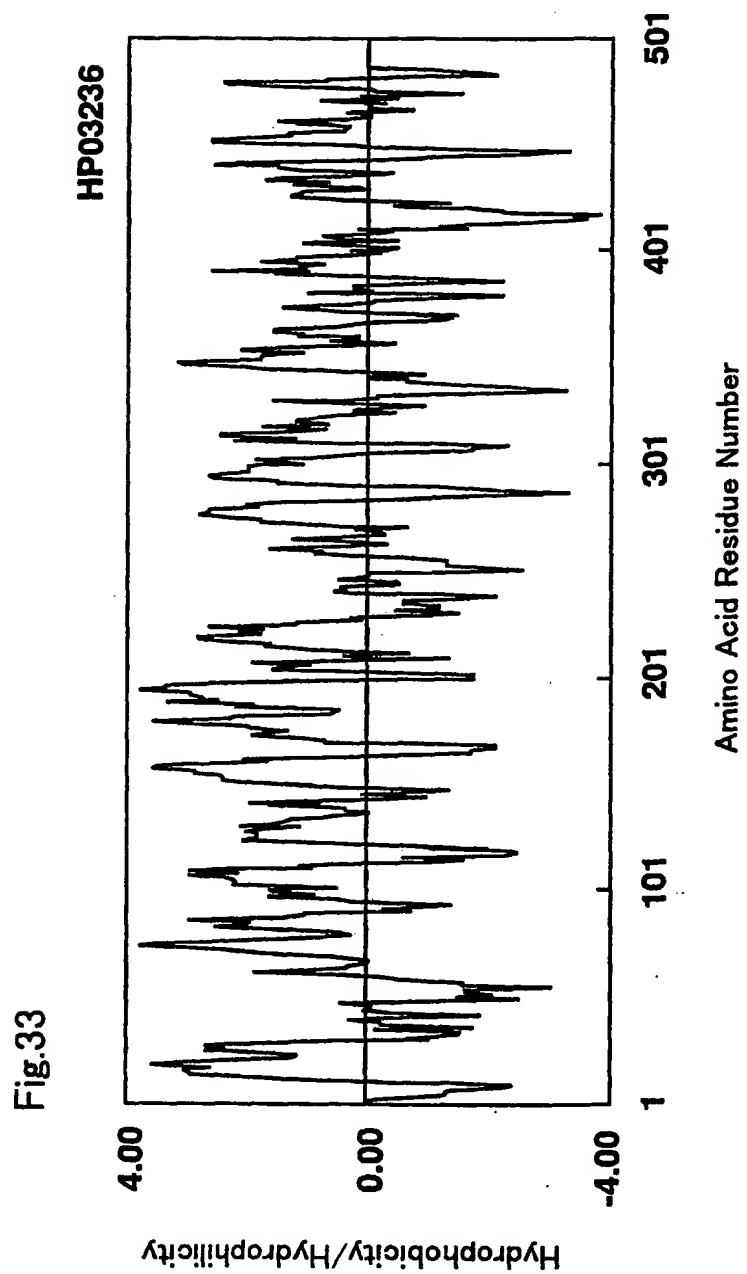
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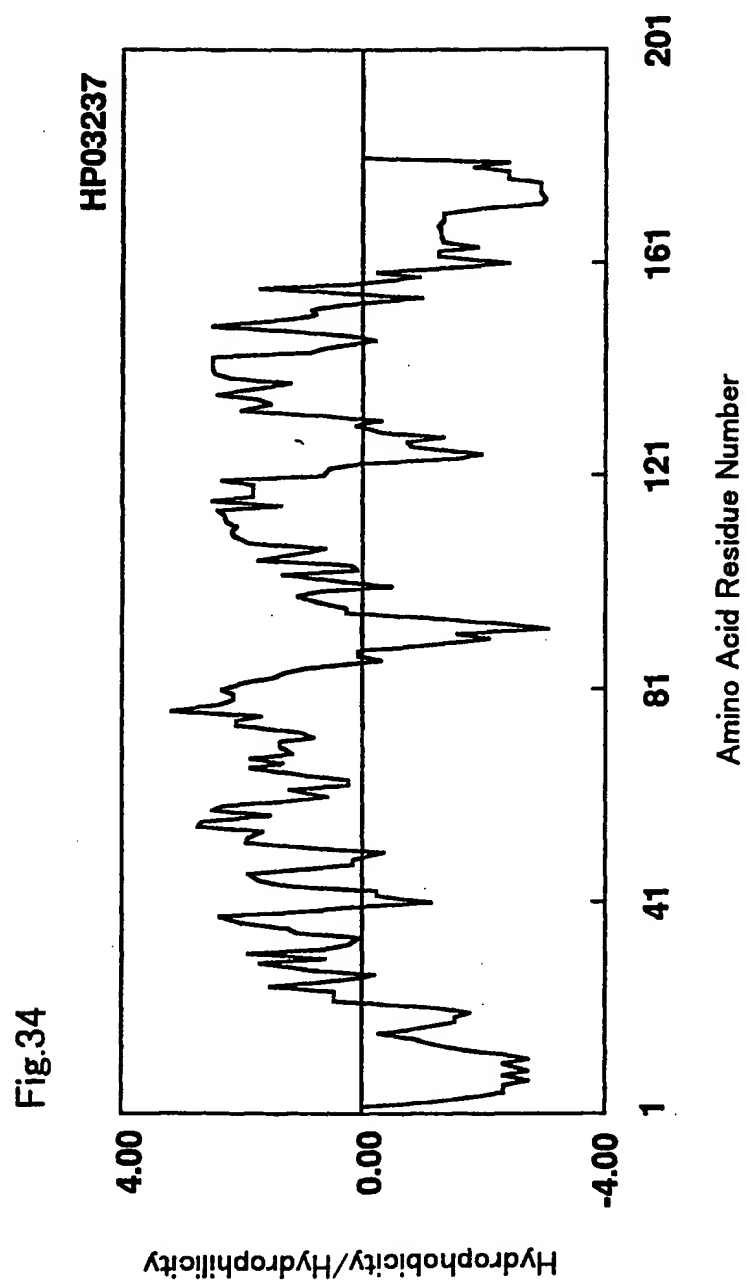
32/50



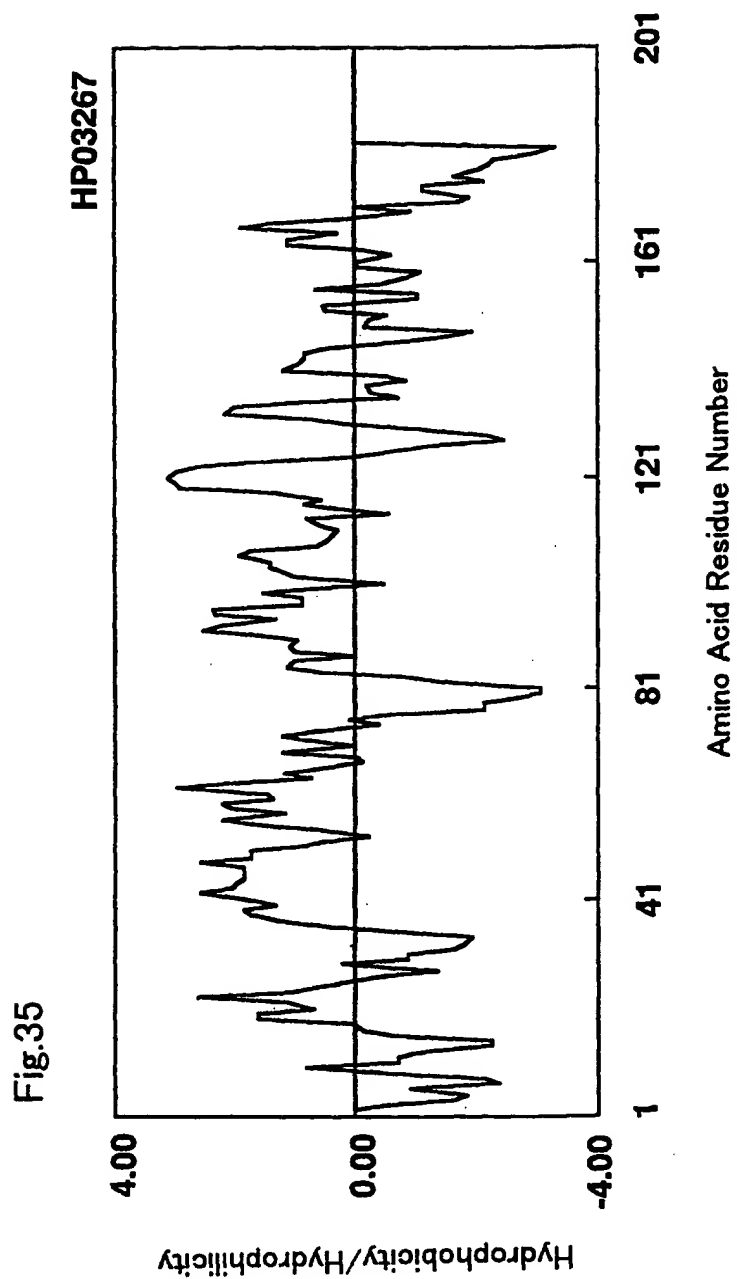
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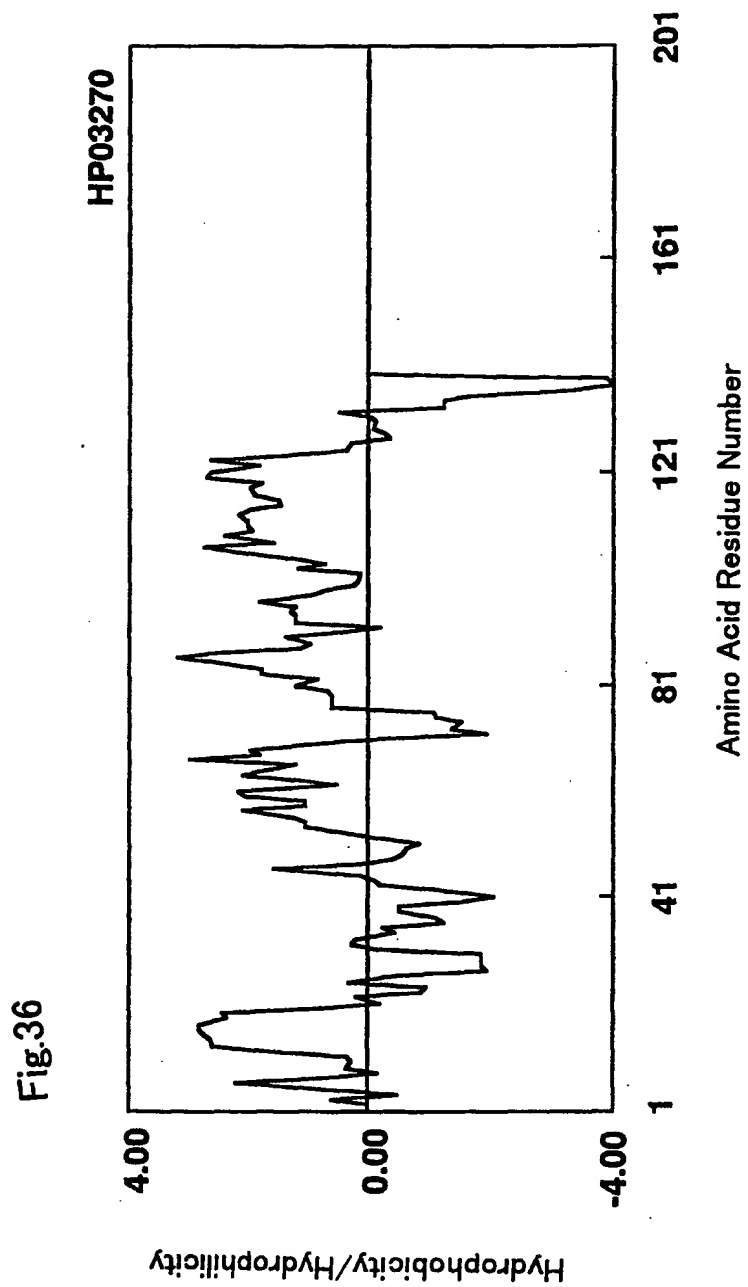
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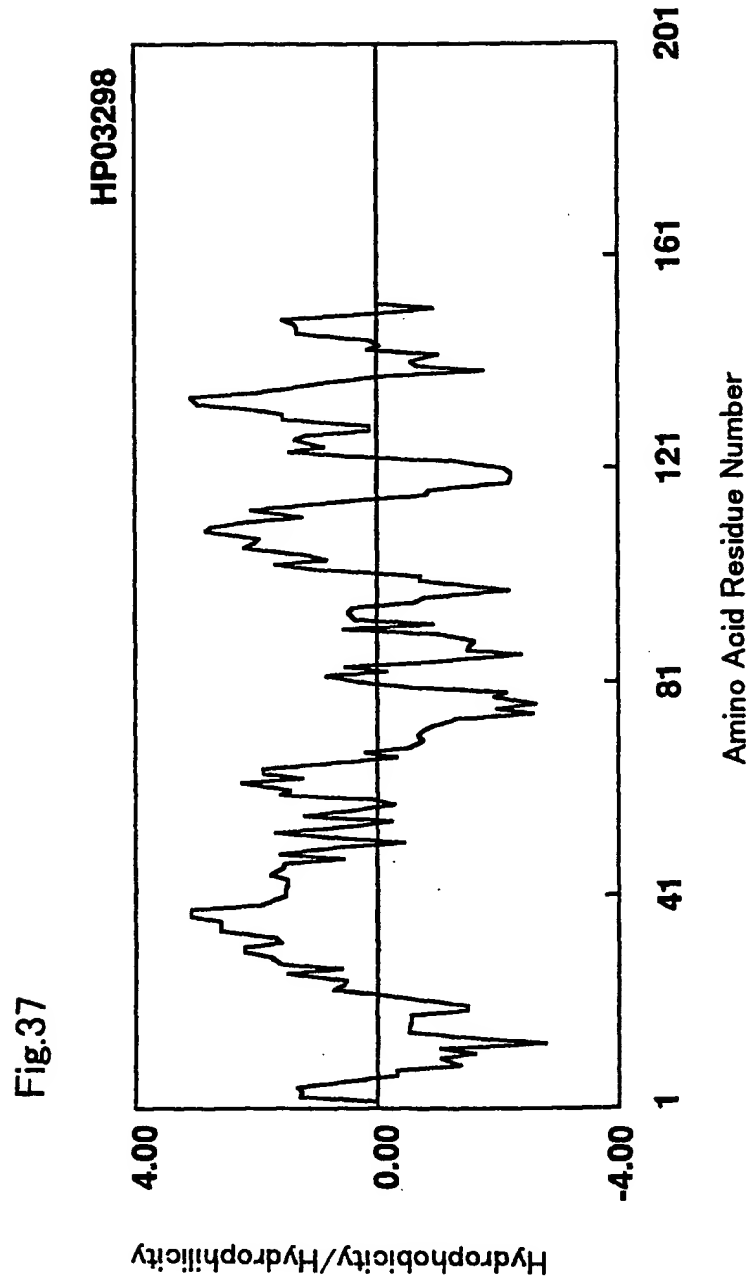
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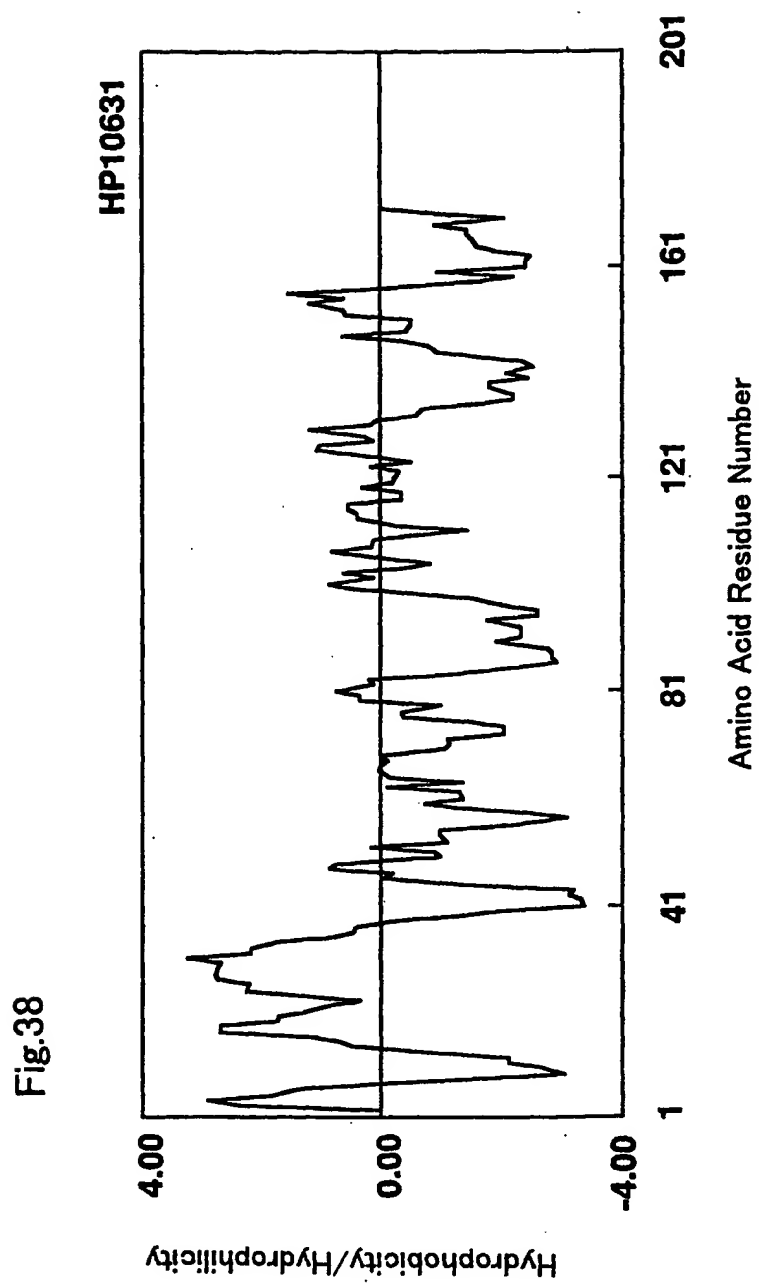
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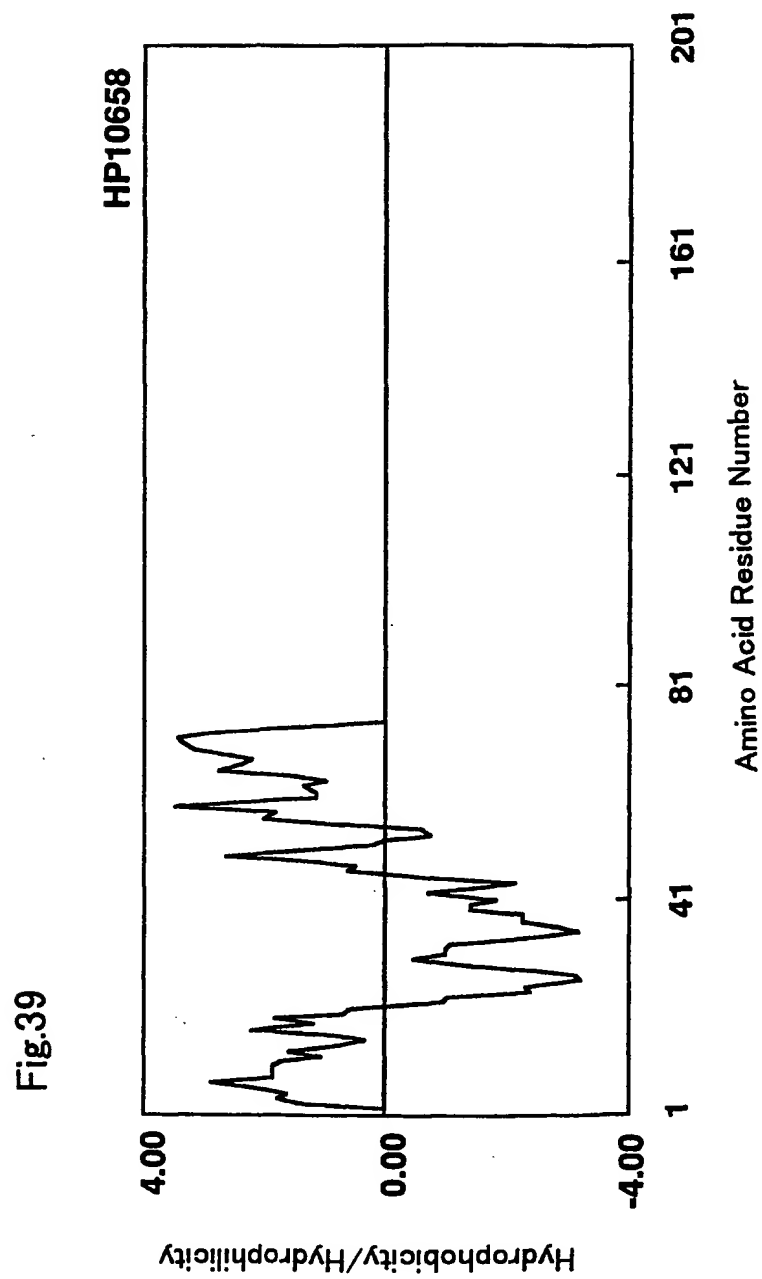
37/50



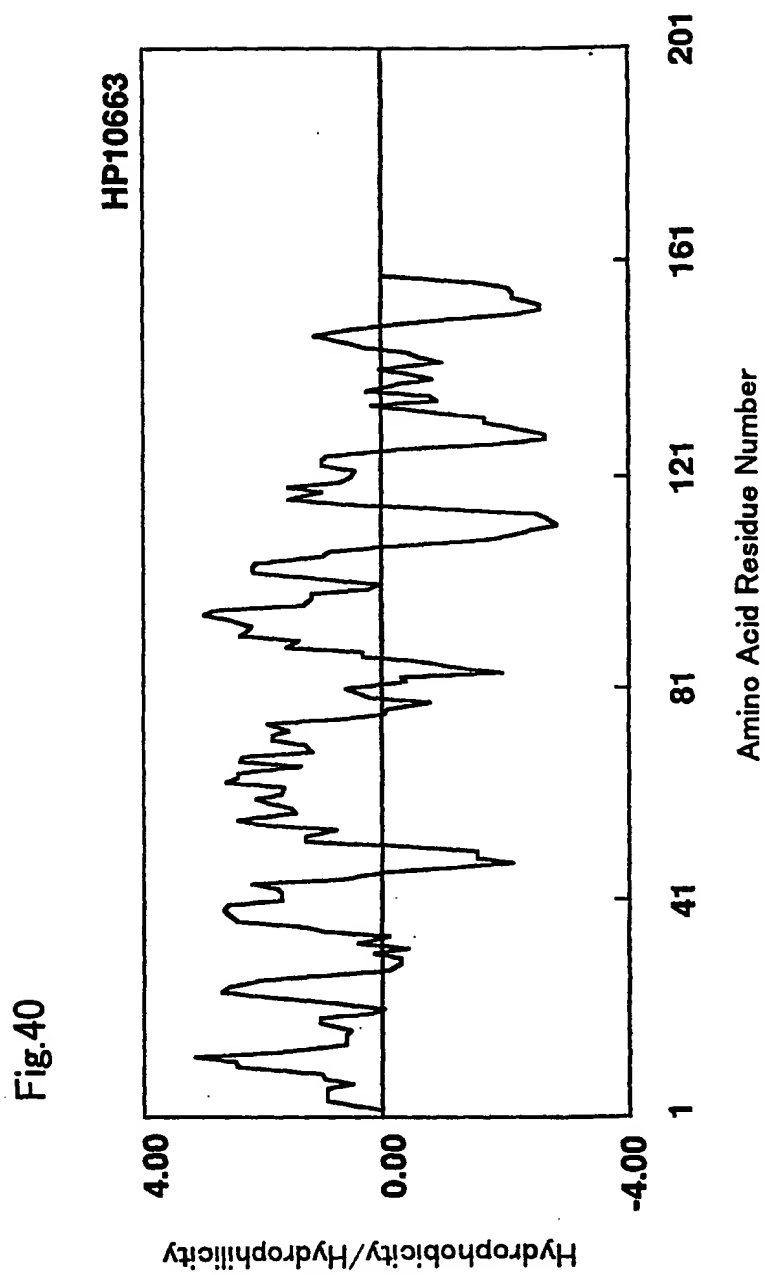
38/50



39/50

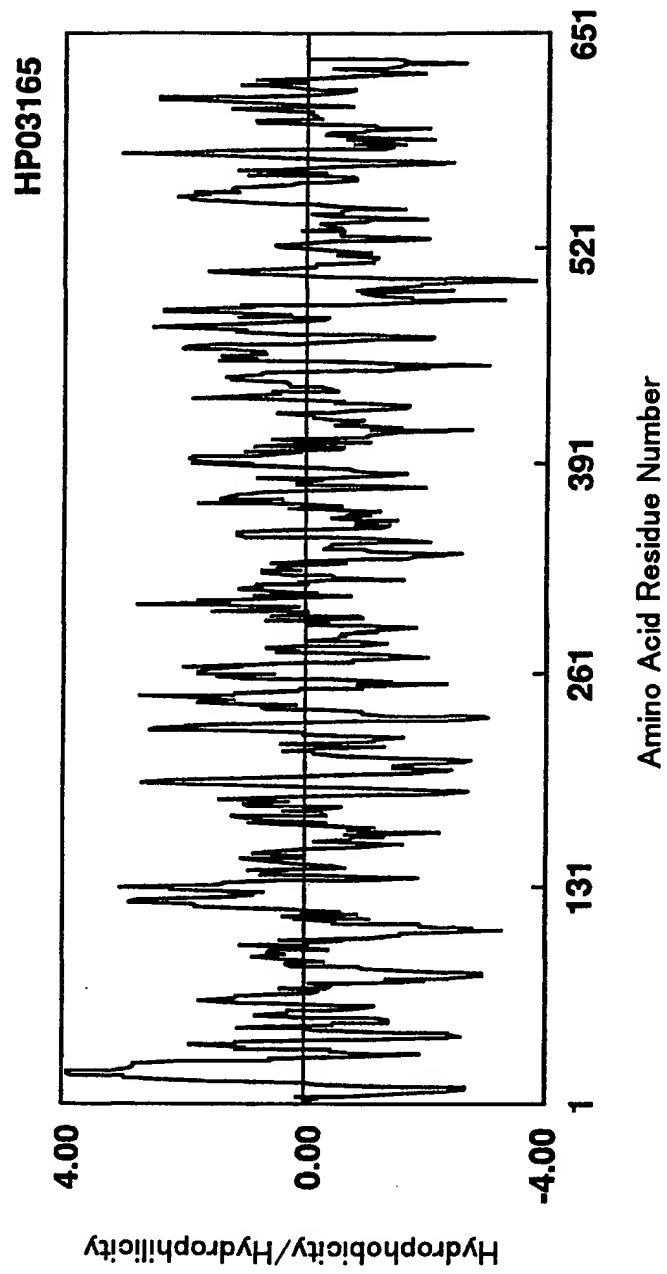


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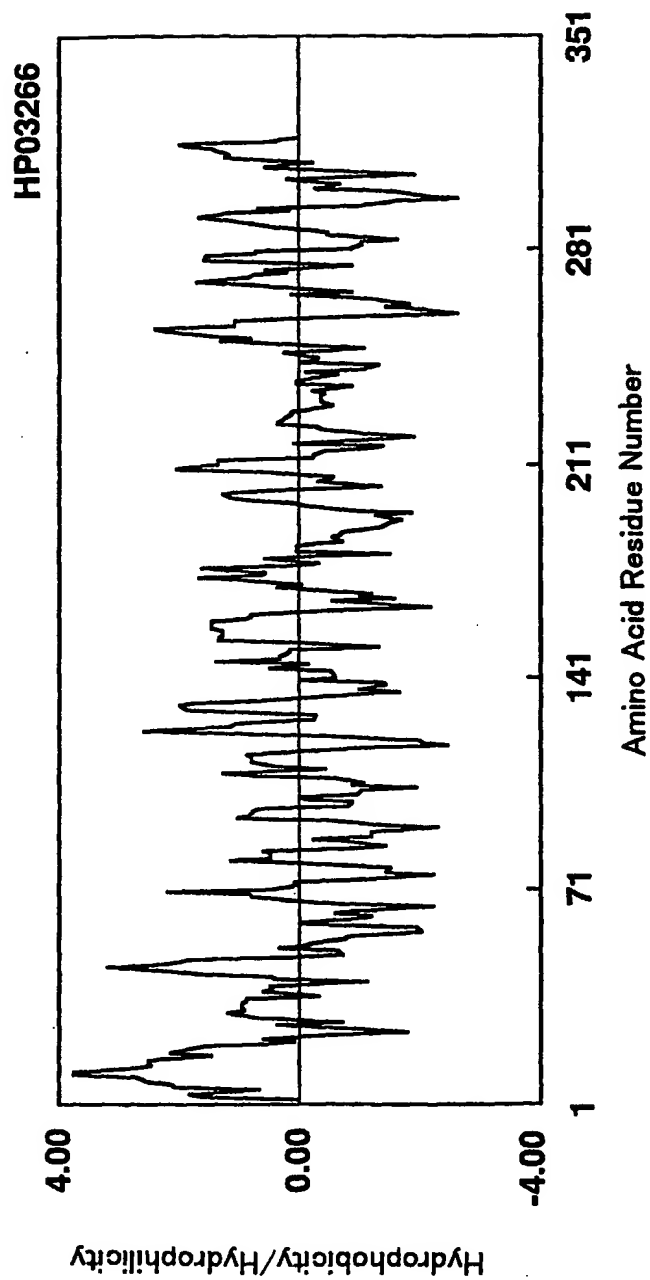
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Fig.41

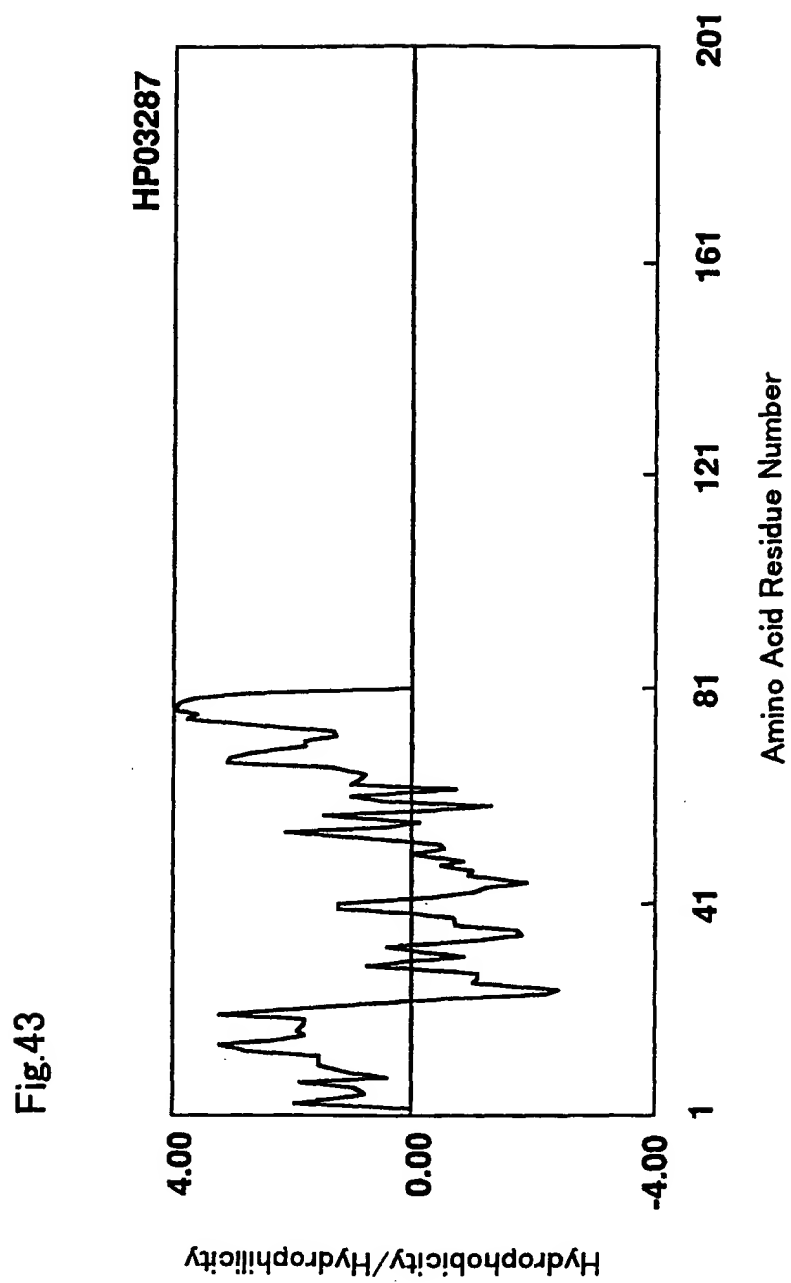


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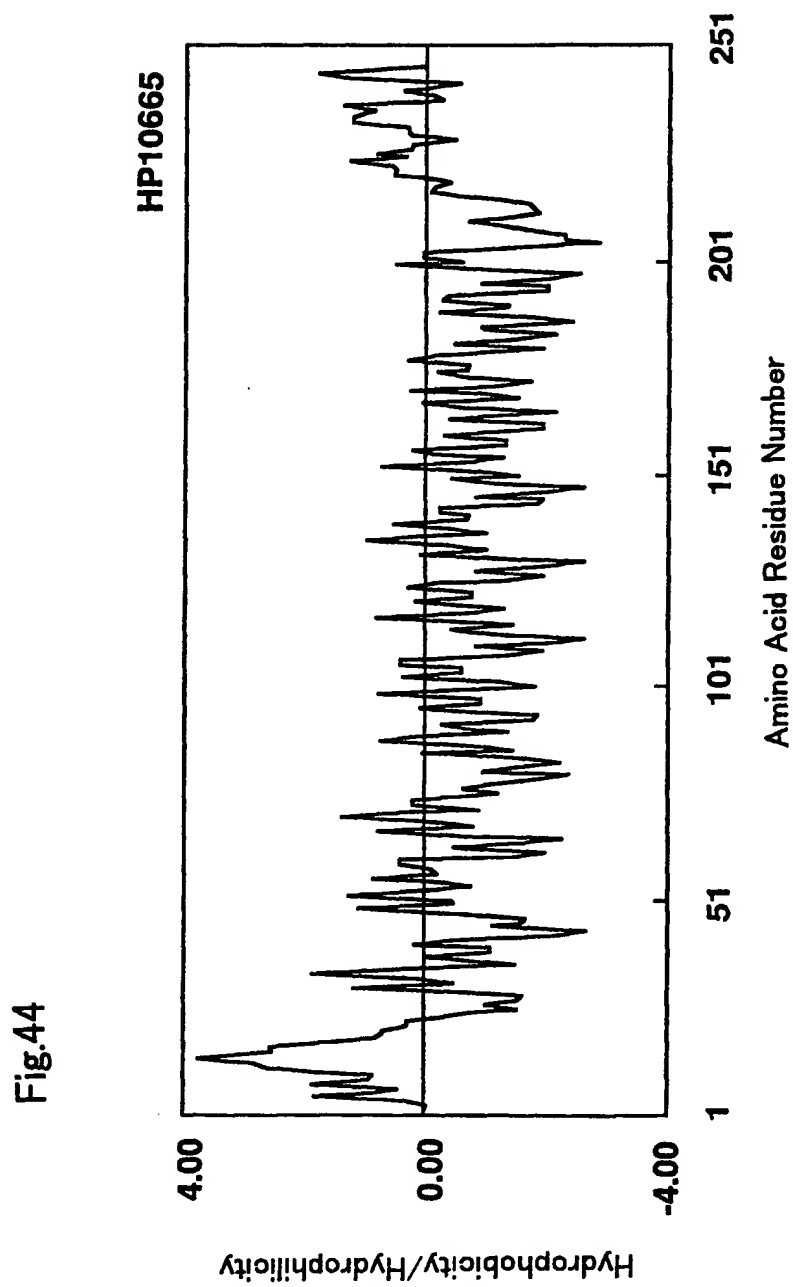
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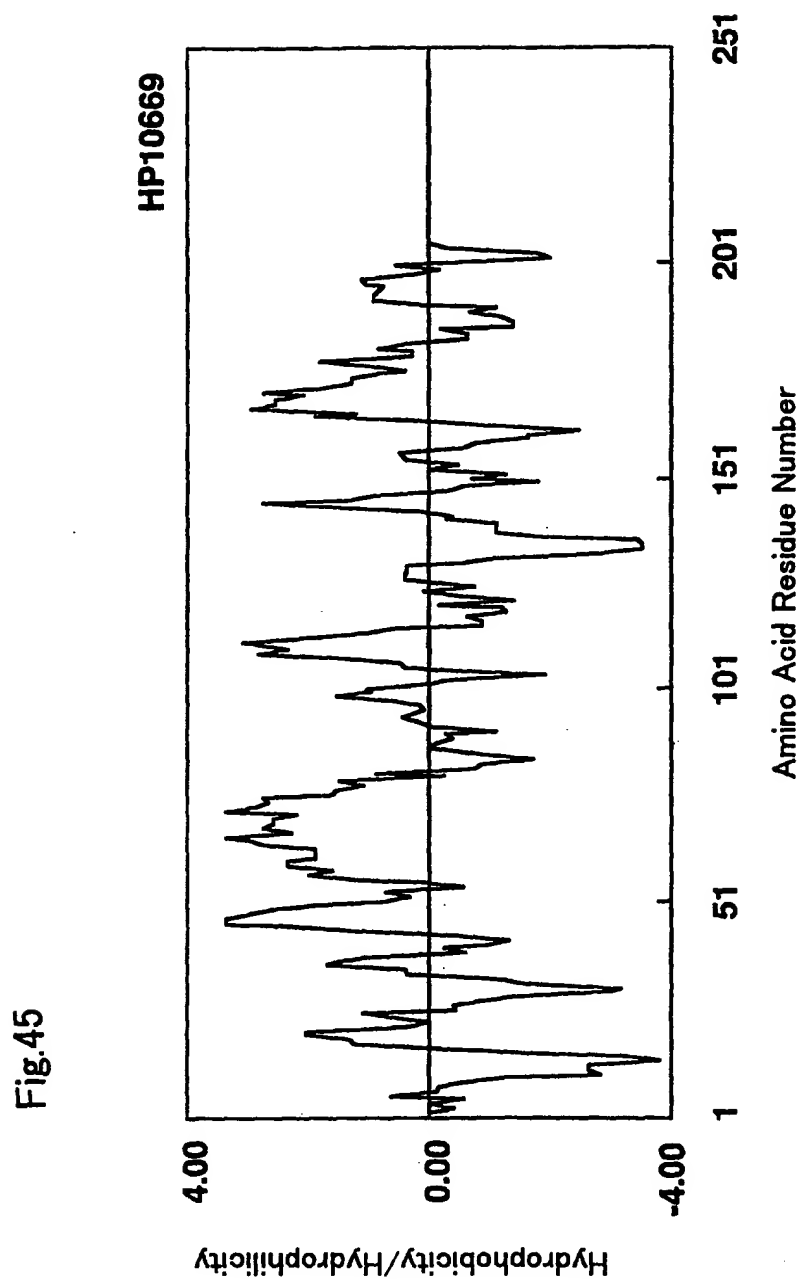
43/50



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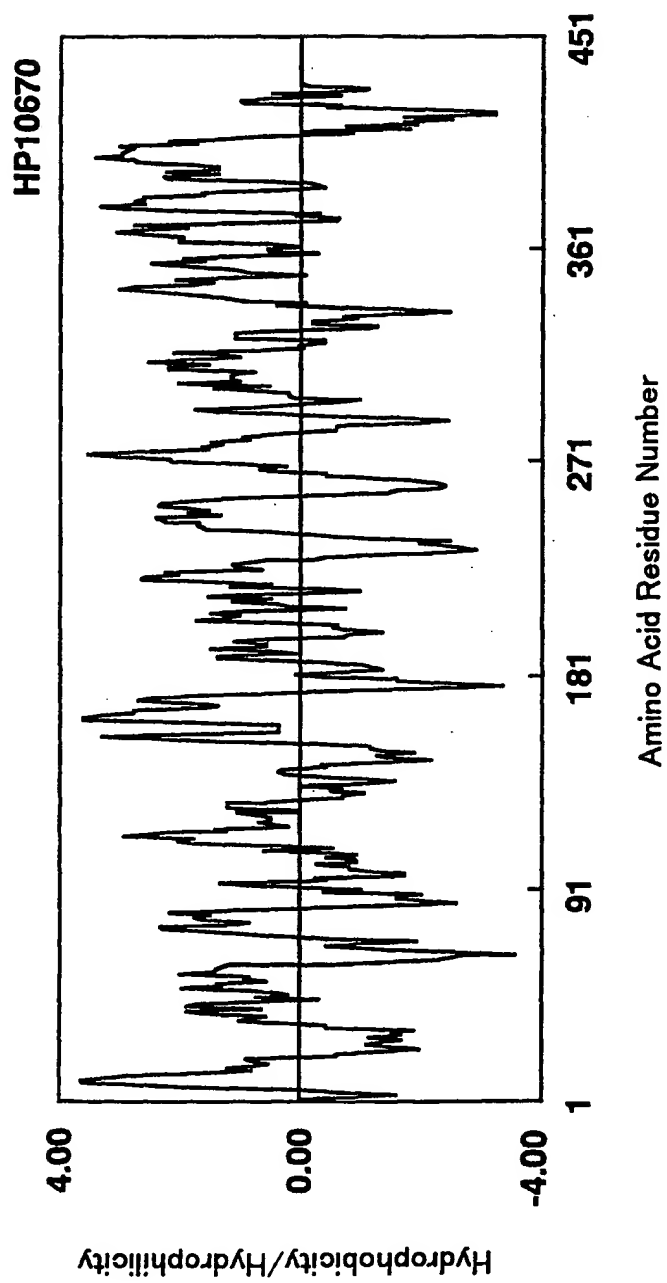


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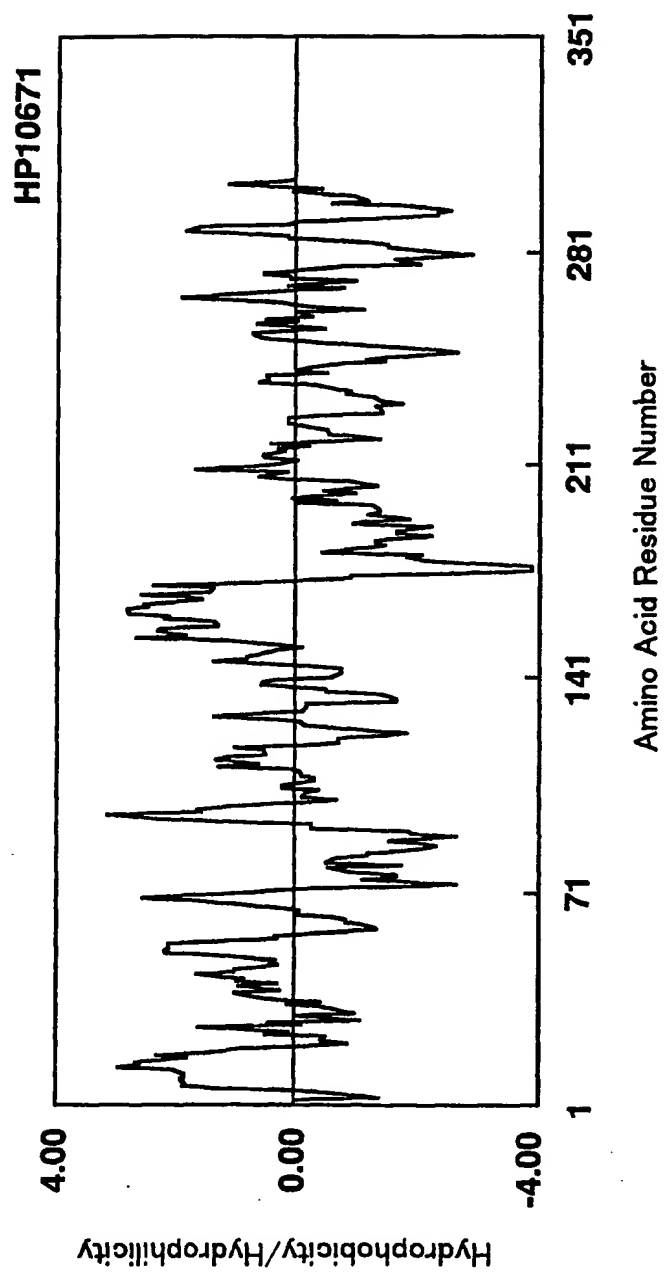
46/50

Fig.46



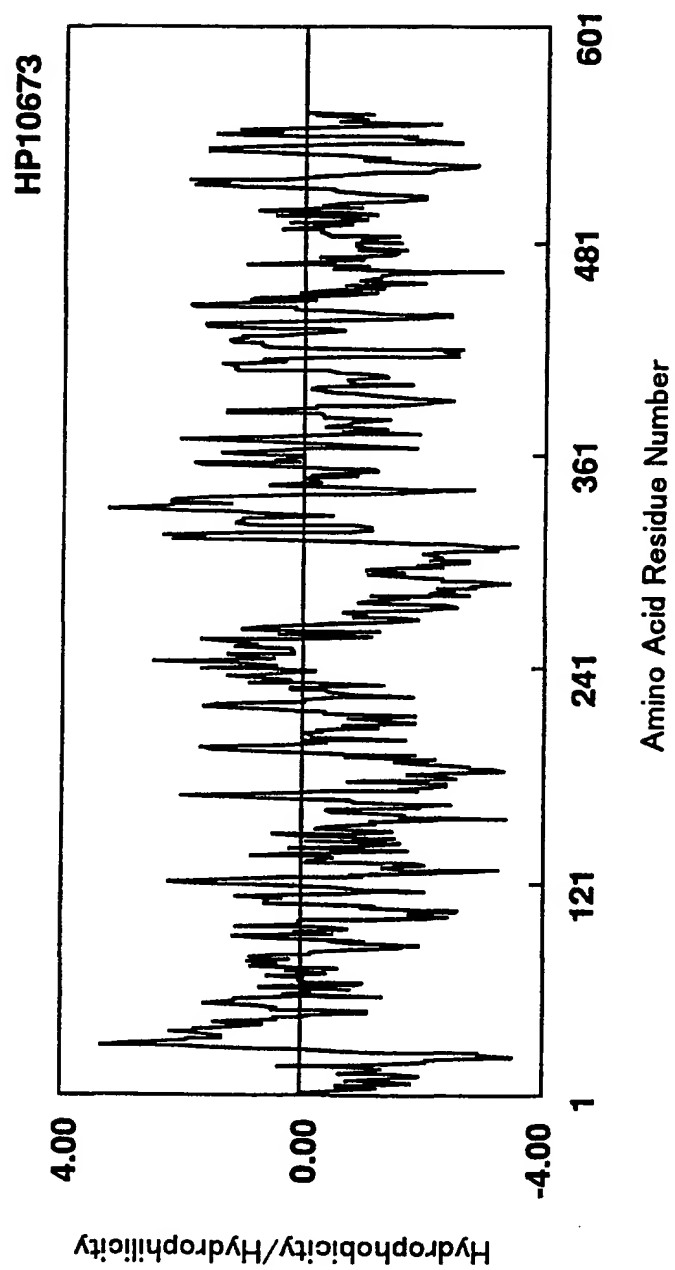
47/50

Fig.47



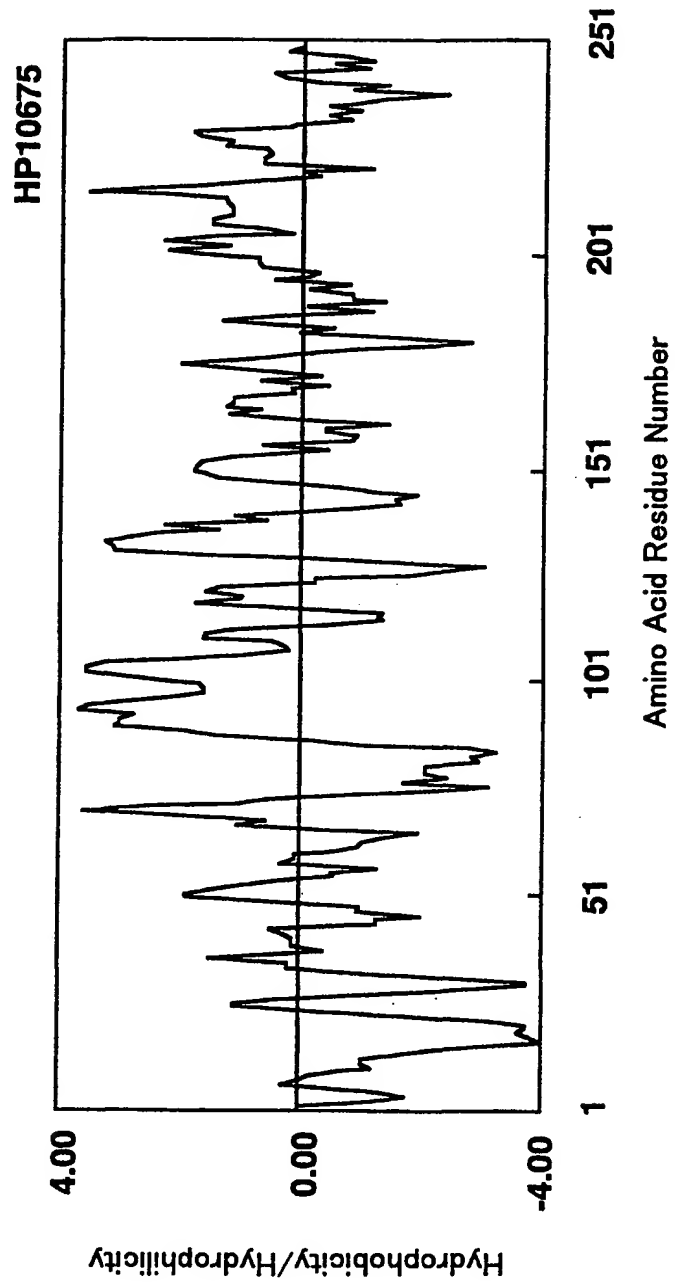
48/50

Fig.48



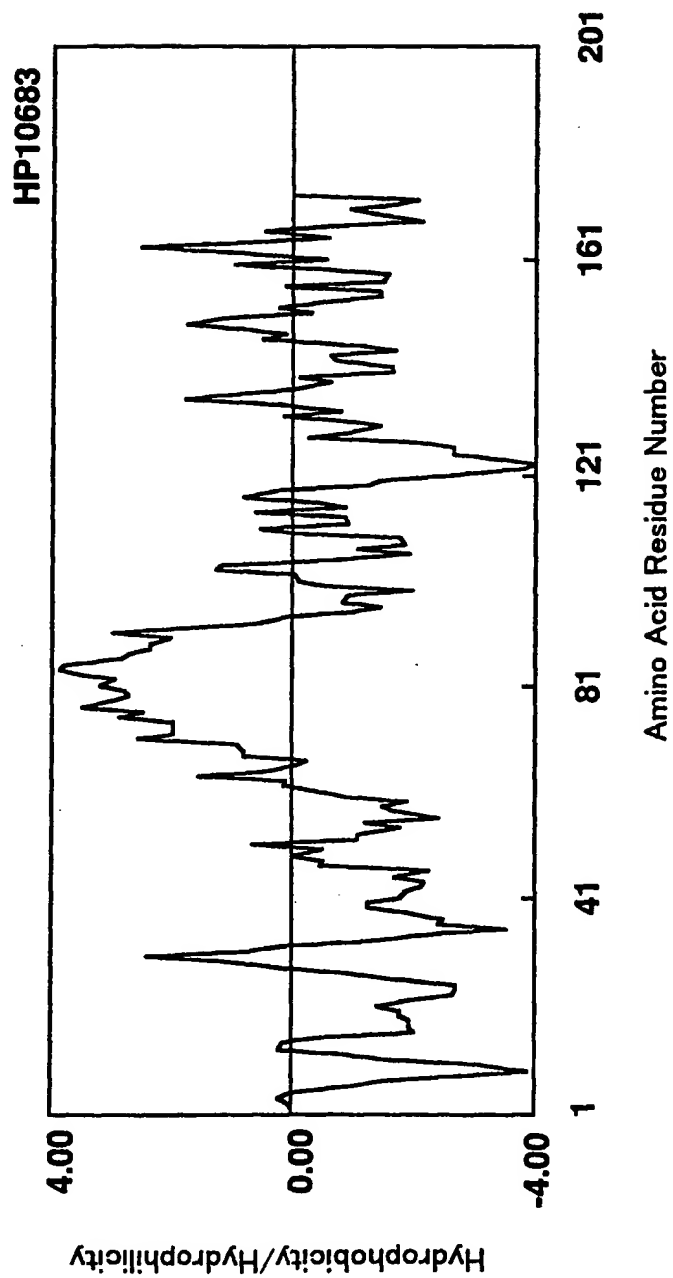
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Fig.49



50/50

Fig.50



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Protegene Inc.

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<130> 661607

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<151> 1998-11-17

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<150> JP 11-69811

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<151> 1999-04-27

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<213> Homo sapiens

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10

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Ala Ser Trp Glu Leu Cys Ala Gly Ala Leu Ser Ala Arg Leu Thr Glu

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Glu Gly Ser Gly Asp Ala Gly Gly Arg Arg Arg Pro Pro Val Asp Pro					
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Arg Arg Leu Ala Arg Gln Leu Leu Leu Leu Leu Trp Leu Leu Glu Ala					
50		55		60	
Pro Leu Leu Leu Gly Val Arg Ala Gln Ala Ala Gly Gln Gly Pro Gly					
65		70		75	80
Gln Gly Pro Gly Pro Gly Gln Gln Pro Pro Pro Pro Pro Gln Gln Gln					
	85		90		95
Gln Ser Gly Gln Gln Tyr Asn Gly Glu Arg Gly Ile Ser Val Pro Asp					
100		105		110	
His Gly Tyr Cys Gln Pro Ile Ser Ile Pro Leu Cys Thr Asp Ile Ala					
115		120		125	
Tyr Asn Gln Thr Ile Met Pro Asn Leu Leu Gly His Thr Asn Gln Glu					
130		135		140	
Asp Ala Gly Leu Glu Val His Gln Phe Tyr Pro Leu Val Lys Val Gln					
145		150		155	160
Cys Ser Ala Glu Leu Lys Phe Phe Leu Cys Ser Met Tyr Ala Pro Val					
	165		170		175
Cys Thr Val Leu Glu Gln Ala Leu Pro Pro Cys Arg Ser Leu Cys Glu					
180		185		190	
Arg Ala Arg Gln Gly Cys Glu Ala Leu Met Asn Lys Phe Gly Phe Gln					
195		200		205	
Trp Pro Asp Thr Leu Lys Cys Glu Lys Phe Pro Val His Gly Ala Gly					
210		215		220	
Glu Leu Cys Val Gly Gln Asn Thr Ser Asp Lys Gly Thr Pro Thr Pro					
225		230		235	240
Ser Leu Leu Pro Glu Phe Trp Thr Ser Asn Pro Gln His Gly Gly Gly					
	245		250		255
Gly His Arg Gly Gly Phe Pro Gly Gly Ala Gly Ala Ser Glu Arg Gly					
260		265		270	
Lys Phe Ser Cys Pro Arg Ala Leu Lys Val Pro Ser Tyr Leu Asn Tyr					
275		280		285	
His Phe Leu Gly Glu Lys Asp Cys Gly Ala Pro Cys Glu Pro Thr Lys					
290		295		300	

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Val Tyr Gly Leu Met Tyr Phe Gly Pro Glu Glu Leu Arg Phe Ser Arg
 305 310 315 320
 Thr Trp Ile Gly Ile Trp Ser Val Leu Cys Cys Ala Ser Thr Leu Phe
 325 330 335
 Thr Val Leu Thr Tyr Leu Val Asp Met Arg Arg Phe Ser Tyr Pro Glu
 340 345 350
 Arg Pro Ile Ile Phe Leu Ser Gly Cys Tyr Thr Ala Val Ala Val Ala
 355 360 365
 Tyr Ile Ala Gly Phe Leu Leu Glu Asp Arg Val Val Cys Asn Asp Lys
 370 375 380
 Phe Ala Glu Asp Gly Ala Arg Thr Val Ala Gln Gly Thr Lys Lys Glu
 385 390 395 400
 Gly Cys Thr Ile Leu Phe Met Met Leu Tyr Phe Phe Ser Met Ala Ser
 405 410 415
 Ser Ile Trp Trp Val Ile Leu Ser Leu Thr Trp Phe Leu Ala Ala Gly
 420 425 430
 Met Lys Trp Gly His Glu Ala Ile Glu Ala Asn Ser Gln Tyr Phe His
 435 440 445
 Leu Ala Ala Trp Ala Val Pro Ala Ile Lys Thr Ile Thr Ile Leu Ala
 450 455 460
 Leu Gly Gln Val Asp Gly Asp Val Leu Ser Gly Val Cys Phe Val Gly
 465 470 475 480
 Leu Asn Asn Val Asp Ala Leu Arg Gly Phe Val Leu Ala Pro Leu Phe
 485 490 495
 Val Tyr Leu Phe Ile Gly Thr Ser Phe Leu Leu Ala Gly Phe Val Ser
 500 505 510
 Leu Phe Arg Ile Arg Thr Ile Met Lys His Asp Gly Thr Lys Thr Glu
 515 520 525
 Lys Leu Glu Lys Leu Met Val Arg Ile Gly Val Phe Ser Val Leu Tyr
 530 535 540
 Thr Val Pro Ala Thr Ile Val Ile Ala Cys Tyr Phe Tyr Glu Gln Ala
 545 550 555 560
 Phe Arg Asp Gln Trp Glu Arg Ser Trp Val Ala Gln Ser Cys Lys Ser
 565 570 575
 Tyr Ala Ile Pro Cys Pro His Leu Gln Ala Gly Gly Gly Ala Pro Pro

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580 585 590
 His Pro Pro Met Ser Pro Asp Phe Thr Val Phe Met Ile Lys Tyr Leu
 595 600 605
 Met Thr Leu Ile Val Gly Ile Thr Ser Gly Phe Trp Ile Trp Ser Gly
 610 615 620
 Lys Thr Leu Asn Ser Trp Arg Lys Phe Tyr Thr Arg Leu Thr Asn Ser
 625 630 635 640
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<212> PRT

<213> Homo sapiens

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 20 25 30
 Asn Ala Ser Met Asp Phe Ala Asp Leu Pro Ala Leu Phe Gly Ala Thr
 35 40 45
 Leu Ser Gln Glu Gly Leu Gln Gly Phe Leu Val Glu Ala His Pro Asp
 50 55 60
 Asn Ala Cys Ser Pro Ile Ala Pro Pro Pro Pro Ala Pro Val Asn Gly
 65 70 75 80
 Ser Val Phe Ile Ala Leu Leu Arg Arg Phe Asp Cys Asn Phe Asp Leu
 85 90 95
 Lys Val Leu Asn Ala Gln Lys Ala Gly Tyr Gly Ala Ala Val Val His
 100 105 110
 Asn Val Asn Ser Asn Glu Leu Leu Asn Met Val Trp Asn Ser Glu Glu
 115 120 125
 Ile Gln Gln Gln Ile Trp Ile Pro Ser Val Phe Ile Gly Glu Arg Ser
 130 135 140
 Ser Glu Tyr Leu Arg Ala Leu Phe Val Tyr Glu Lys Gly Ala Arg Val
 145 150 155 160

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Leu Leu Val Pro Asp Asn Thr Phe Pro Leu Gly Tyr Tyr Leu Ile Pro
 165 170 175
 Phe Thr Gly Ile Val Gly Leu Leu Val Leu Ala Met Gly Ala Val Met
 180 185 190
 Ile Ala Arg Cys Ile Gln His Arg Lys Arg Leu Gln Arg Asn Arg Leu
 195 200 205
 Thr Lys Glu Gln Leu Lys Gln Ile Pro Thr His Asp Tyr Gln Lys Gly
 210 215 220
 Asp Gln Tyr Asp Val Cys Ala Ile Cys Leu Asp Glu Tyr Glu Asp Gly
 225 230 235 240
 Asp Lys Leu Arg Val Leu Pro Cys Ala His Ala Tyr His Ser Arg Cys
 245 250 255
 Val Asp Pro Trp Leu Thr Gln Thr Arg Lys Thr Cys Pro Ile Cys Lys
 260 265 270
 Gln Pro Val His Arg Gly Pro Gly Asp Glu Asp Gln Glu Glu Thr
 275 280 285
 Gln Gly Gln Glu Glu Gly Asp Glu Gly Glu Pro Arg Asp His Pro Ala
 290 295 300
 Ser Glu Arg Thr Pro Leu Leu Gly Ser Ser Pro Thr Leu Pro Thr Ser
 305 310 315 320
 Phe Gly Ser Leu Ala Pro Ala Pro Leu Val Phe Pro Gly Pro Ser Thr
 325 330 335
 Asp Pro Pro Leu Ser Pro Pro Ser Ser Pro Val Ile Leu Val
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<211> 206

<212> PRT

<213> Homo sapiens

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 20 25 30
 Phe Leu Leu Tyr Tyr Val Asp Thr Phe Val Ser Val Tyr Lys Ile Asn

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35	40	45
Lys Met Ala Phe Trp Val Gly Glu Thr Val Phe Leu Leu Trp Asn Ser		
50	55	60
Leu Asn Asp Pro Leu Phe Gly Trp Leu Ser Asp Arg Gln Phe Leu Ser		
65	70	75
Ser Gln Pro Arg Gly Arg Asp Leu Pro Trp Leu Gly Leu Val Gly Pro		
85	90	95
Ser Gly Leu Trp Thr Ala Asn Thr Leu Cys Cys Phe Trp Lys Ile Pro		
100	105	110
Leu Pro His Pro Cys Leu Ser Pro Ser Ser Pro Pro Thr Leu Arg Ser		
115	120	125
Gly His Pro Ile Pro Phe Gly His Gln Pro Asn Arg Leu Ile Arg Gly		
130	135	140
Trp Lys Leu Gly Gln Arg Arg Arg Val Tyr Pro Leu Val Arg Arg Arg		
145	150	155
Ala Leu Leu Lys Gly Cys Gly Ala Gly Pro Gly Ala Gly Pro Gly Leu		
165	170	175
Ala Trp Ala Ala Ala Gly Ala Val Val Pro Gly Val Leu Gly Ala Leu		
180	185	190
Gly Pro Ser Trp Pro Ala Val Leu Ala Val Pro Val Pro Leu		
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<213> Homo sapiens

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Met His Tyr Tyr Arg Tyr Ser Asn Ala Lys Val Ser Cys Trp Tyr Lys		
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Tyr Leu Leu Phe Ser Tyr Asn Ile Ile Phe Trp Leu Ala Gly Val Val		
20	25	30
Phe Leu Gly Val Gly Leu Trp Ala Trp Ser Glu Lys Gly Val Leu Ser		
35	40	45
Asp Leu Thr Lys Val Thr Arg Met His Gly Ile Asp Pro Val Val Leu		
50	55	60

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Val Leu Met Val Gly Val Val Met Phe Thr Leu Gly Phe Ala Gly Cys
 65 70 75 80
 Val Gly Ala Leu Arg Glu Asn Ile Cys Leu Leu Asn Phe Asn Gln Cys
 85 90 95
 Cys Gly Ala Tyr Gly Pro Glu Asp Trp Asp Leu Asn Val Tyr Phe Asn
 100 105 110
 Cys Ser Gly Ala Ser Tyr Ser Arg Glu Lys Cys Gly Val Pro Phe Ser
 115 120 125
 Cys Cys Val Pro Asp Pro Ala Gln Lys Val Val Asn Thr Gln Cys Gly
 130 135 140
 Tyr Asp Val Arg Ile Gln Leu Lys Ser Lys Trp Asp Glu Ser Ile Phe
 145 150 155 160
 Thr Lys Gly Cys Ile Gln Ala Leu Glu Ser Trp Leu Pro Arg Asn Ile
 165 170 175
 Tyr Ile Val Ala Gly Val Phe Ile Ala Ile Ser Leu Leu Gln Ile Phe
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 Gly Ile Phe Leu Ala Arg Thr Leu Ile Ser Asp Ile Glu Ala Val Lys
 195 200 205
 Ala Gly His His Phe
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<210> 5

<211> 595

<212> PRT

<213> Homo sapiens

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 20 25 30
 Val Val Leu Ala Ile Leu Ala Arg Asn Ala Glu His Ser Leu Pro His
 35 40 45
 Tyr Leu Gly Ala Leu Glu Arg Leu Asp Tyr Pro Arg Ala Arg Met Ala
 50 55 60
 Leu Trp Cys Ala Thr Asp His Asn Val Asp Asn Thr Thr Glu Met Leu

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65	70	75	80
Gln Glu Trp Leu Ala Ala Val Gly Asp Asp Tyr Ala Ala Val Val Trp			
85	90	95	
Arg Pro Glu Gly Glu Pro Arg Phe Tyr Pro Asp Glu Glu Gly Pro Lys			
100	105	110	
His Trp Thr Lys Glu Arg His Gln Phe Leu Met Glu Leu Lys Gln Glu			
115	120	125	
Ala Leu Thr Phe Ala Arg Asn Trp Gly Ala Asp Tyr Ile Leu Phe Ala			
130	135	140	
Asp Thr Asp Asn Ile Leu Thr Asn Asn Gln Thr Leu Arg Leu Leu Met			
145	150	155	160
Gly Gln Gly Leu Pro Val Val Ala Pro Met Leu Asp Ser Gln Thr Tyr			
165	170	175	
Tyr Ser Asn Phe Trp Cys Gly Ile Thr Pro Gln Gly Tyr Tyr Arg Arg			
180	185	190	
Thr Ala Glu Tyr Phe Pro Thr Lys Asn Arg Gln Arg Arg Gly Cys Phe			
195	200	205	
Arg Val Pro Met Val His Ser Thr Phe Leu Ala Ser Leu Arg Ala Glu			
210	215	220	
Gly Ala Asp Gln Leu Ala Phe Tyr Pro Pro His Pro Asn Tyr Thr Trp			
225	230	235	240
Pro Phe Asp Asp Ile Ile Val Phe Ala Tyr Ala Cys Gln Ala Ala Gly			
245	250	255	
Val Ser Val His Val Cys Asn Glu His Arg Tyr Gly Tyr Met Asn Val			
260	265	270	
Pro Val Lys Ser His Gln Gly Leu Glu Asp Glu Arg Val Asn Phe Ile			
275	280	285	
His Leu Ile Leu Glu Ala Leu Val Asp Gly Pro Arg Met Gln Ala Ser			
290	295	300	
Ala His Val Thr Arg Pro Ser Lys Arg Pro Ser Lys Ile Gly Phe Asp			
305	310	315	320
Glu Val Phe Val Ile Ser Leu Ala Arg Arg Pro Asp Arg Arg Glu Arg			
325	330	335	
Met Leu Ala Ser Leu Trp Glu Met Glu Ile Ser Gly Arg Val Val Asp			
340	345	350	

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 355 360 365
 Val Asp Leu Leu Pro Gly Tyr Gln Asp Pro Tyr Ser Gly Arg Thr Leu
 370 375 380
 Thr Lys Gly Glu Val Gly Cys Phe Leu Ser His Tyr Ser Ile Trp Glu
 385 390 395 400
 Glu Val Val Ala Arg Gly Leu Ala Arg Val Leu Val Phe Glu Asp Asp
 405 410 415
 Val Arg Phe Glu Ser Asn Phe Arg Gly Arg Leu Glu Arg Leu Met Glu
 420 425 430
 Asp Val Glu Ala Glu Lys Leu Ser Trp Asp Leu Ile Tyr Leu Gly Arg
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 500 505 510
 Glu Gln Tyr Lys Ala His Phe Trp Pro Arg Asp Leu Val Ala Phe Ser
 515 520 525
 Ala Gln Pro Leu Leu Ala Ala Pro Thr His Tyr Ala Gly Asp Ala Glu
 530 535 540
 Trp Leu Ser Asp Thr Glu Thr Ser Ser Pro Trp Asp Asp Asp Ser Gly
 545 550 555 560
 Arg Leu Ile Ser Trp Ser Gly Ser Gln Lys Thr Leu Arg Ser Pro Arg
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<210> 6

<211> 264

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<212> PRT

<213> Homo sapiens

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Cys Glu Ser Gly His Cys Cys Gly Glu Thr Gly Cys Cys Thr Tyr Tyr
      35             40             45
Tyr Glu Leu Trp Trp Phe Trp Leu Leu Trp Thr Val Leu Ile Leu Phe
      50             55             60
Ser Cys Cys Cys Ala Phe Arg His Arg Arg Ala Lys Leu Arg Leu Gln
      65             70             75             80
Gln Gln Gln Arg Gln Arg Glu Ile Asn Leu Leu Ala Tyr His Gly Ala
      85             90             95
Cys His Gly Ala Gly Pro Phe Pro Thr Gly Ser Leu Leu Asp Leu Arg
      100            105            110
Phe Leu Ser Thr Phe Lys Pro Pro Ala Tyr Glu Asp Val Val His Arg
      115            120            125
Pro Gly Thr Pro Pro Pro Pro Tyr Thr Val Ala Pro Gly Arg Pro Leu
      130            135            140
Thr Ala Ser Ser Glu Gln Thr Cys Cys Ser Ser Ser Ser Ser Cys Pro
      145            150            155            160
Ala His Phe Glu Gly Thr Asn Val Glu Gly Val Ser Ser His Gln Ser
      165            170            175
Ala Pro Pro His Gln Glu Gly Glu Pro Gly Ala Gly Val Thr Pro Ala
      180            185            190
Ser Thr Pro Pro Ser Cys Arg Tyr Arg Arg Leu Thr Gly Asp Ser Gly
      195            200            205
Ile Glu Leu Cys Pro Cys Pro Ala Ser Gly Glu Gly Glu Pro Val Lys
      210            215            220
Glu Val Arg Val Ser Ala Thr Leu Pro Asp Leu Glu Asp Tyr Ser Pro
      225            230            235            240
Cys Ala Leu Pro Pro Glu Ser Val Pro Gln Ile Phe Pro Met Gly Leu
      245            250            255

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Ser Ser Ser Glu Gly Asp Ile Pro

260

<210> 7

<211> 343

<212> PRT

<213> Homo sapiens

<400> 7

Met Gln Pro Pro Pro Pro Gly Pro Leu Gly Asp Cys Leu Arg Asp Trp

1 5 10 15

Glu Asp Leu Gln Gln Asp Phe Gln Asn Ile Gln Glu Thr His Arg Leu

20 25 30

Tyr Arg Leu Lys Leu Glu Glu Leu Thr Lys Leu Gln Asn Asn Cys Thr

35 40 45

Ser Ser Ile Thr Arg Gln Lys Lys Arg Leu Gln Glu Leu Ala Leu Ala

50 55 60

Leu Lys Lys Cys Lys Pro Ser Leu Pro Ala Glu Ala Glu Gly Ala Ala

65 70 75 80

Gln Glu Leu Glu Asn Gln Met Lys Glu Arg Gln Gly Leu Phe Phe Asp

85 90 95

Met Glu Ala Tyr Leu Pro Lys Lys Asn Gly Leu Tyr Leu Ser Leu Val

100 105 110

Leu Gly Asn Val Asn Val Thr Leu Leu Ser Lys Gln Ala Lys Phe Ala

115 120 125

Tyr Lys Asp Glu Tyr Glu Lys Phe Lys Leu Tyr Leu Thr Ile Ile Leu

130 135 140

Ile Leu Ile Ser Phe Thr Cys Arg Phe Leu Leu Asn Ser Arg Val Thr

145 150 155 160

Asp Ala Ala Phe Asn Phe Leu Leu Val Trp Tyr Tyr Cys Thr Leu Thr

165 170 175

Ile Arg Glu Ser Ile Leu Ile Asn Asn Gly Ser Arg Ile Lys Gly Trp

180 185 190

Trp Val Phe His His Tyr Val Ser Thr Phe Leu Ser Gly Val Met Leu

195 200 205

Thr Trp Pro Asp Gly Leu Met Tyr Gln Lys Phe Arg Asn Gln Phe Leu

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210 215 220
 Ser Phe Ser Met Tyr Gln Ser Phe Val Gln Phe Leu Gln Tyr Tyr Tyr
 225 230 235 240
 Gln Ser Gly Cys Leu Tyr Arg Leu Arg Ala Leu Gly Glu Arg His Thr
 245 250 255
 Met Asp Leu Thr Val Glu Gly Phe Gln Ser Trp Met Trp Arg Gly Leu
 260 265 270
 Thr Phe Leu Leu Pro Phe Leu Phe Phe Gly His Phe Trp Gln Leu Phe
 275 280 285
 Asn Ala Leu Thr Leu Phe Asn Leu Ala Gln Asp Pro Gln Cys Lys Glu
 290 295 300
 Trp Gln Val Leu Met Cys Gly Phe Pro Phe Leu Leu Leu Phe Leu Gly
 305 310 315 320
 Asn Phe Phe Thr Thr Leu Arg Val Val His His Lys Phe His Ser Gln
 325 330 335
 Arg His Gly Ser Lys Lys Asp
 340

<210> 8

<211> 244

<212> PRT

<213> Homo sapiens

<400> 8

Met Asp Ile Leu Val Pro Leu Leu Gln Leu Leu Val Leu Leu Leu Thr
 1 5 10 15
 Leu Pro Leu His Leu Met Ala Leu Leu Gly Cys Trp Gln Pro Leu Cys
 20 25 30
 Lys Ser Tyr Phe Pro Tyr Leu Met Ala Val Leu Thr Pro Lys Ser Asn
 35 40 45
 Arg Lys Met Glu Ser Lys Lys Arg Glu Leu Phe Ser Gln Ile Lys Gly
 50 55 60
 Leu Thr Gly Ala Ser Gly Lys Val Ala Leu Leu Glu Leu Gly Cys Gly
 65 70 75 80
 Thr Gly Ala Asn Phe Gln Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys
 85 90 95

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Leu Asp Pro Asn Pro His Phe Glu Lys Phe Leu Thr Lys Ser Met Ala
 100 105 110
 Glu Asn Arg His Leu Gln Tyr Glu Arg Phe Val Val Ala Pro Gly Glu
 115 120 125
 Asp Met Arg Gln Leu Ala Asp Gly Ser Met Asp Val Val Val Cys Thr
 130 135 140
 Leu Val Leu Cys Ser Val Gln Ser Pro Arg Lys Val Leu Gln Glu Val
 145 150 155 160
 Arg Arg Val Leu Arg Pro Gly Gly Val Leu Phe Phe Trp Glu His Val
 165 170 175
 Ala Glu Pro Tyr Gly Ser Trp Ala Phe Met Trp Gln Gln Val Phe Glu
 180 185 190
 Pro Thr Trp Lys His Ile Gly Asp Gly Cys Cys Leu Thr Arg Glu Thr
 195 200 205
 Trp Lys Asp Leu Glu Asn Ala Gln Phe Ser Glu Ile Gln Met Glu Arg
 210 215 220
 Gln Pro Pro Pro Leu Lys Trp Leu Pro Val Gly Pro His Ile Met Gly
 225 230 235 240
 Lys Ala Val Lys

<210> 9

<211> 303

<212> PRT

<213> Homo sapiens

<400> 9

Met Lys Leu Lys Leu Lys Asn Val Phe Leu Ala Tyr Phe Leu Val Ser
 1 5 10 15
 Ile Ala Gly Leu Leu Tyr Ala Leu Val Gln Leu Gly Gln Pro Cys Asp
 20 25 30
 Cys Leu Pro Pro Leu Arg Ala Ala Ala Glu Gln Leu Arg Gln Lys Asp
 35 40 45
 Leu Arg Ile Ser Gln Leu Gln Ala Glu Leu Arg Arg Pro Pro Pro Ala
 50 55 60
 Pro Ala Gln Pro Pro Glu Pro Glu Ala Leu Pro Thr Ile Tyr Val Val

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65	70	75	80
Thr Pro Thr Tyr Ala Arg Pro Leu Trp Val Gln Tyr Pro Gln Asp Val			
85	90	95	
Thr Thr Phe Asn Ile Asp Asp Gln Tyr Leu Leu Gly Asp Ala Leu Leu			
100	105	110	
Val His Pro Val Ser Asp Ser Gly Ala His Gly Val Gln Val Tyr Leu			
115	120	125	
Pro Gly Gln Gly Glu Val Trp Tyr Asp Ile Gln Ser Tyr Gln Lys His			
130	135	140	
His Gly Pro Gln Thr Leu Tyr Leu Pro Val Thr Leu Ser Ser Ile Pro			
145	150	155	160
Val Phe Gln Arg Gly Gly Thr Ile Val Pro Arg Trp Met Arg Val Arg			
165	170	175	
Arg Ser Ser Glu Cys Met Lys Asp Asp Pro Ile Thr Leu Phe Val Ala			
180	185	190	
Leu Ser Pro Gln Gly Thr Ala Gln Gly Glu Leu Phe Leu Asp Asp Gly			
195	200	205	
His Thr Phe Asn Tyr Gln Thr Arg Gln Glu Phe Leu Leu Arg Arg Phe			
210	215	220	
Ser Phe Ser Gly Asn Thr Leu Val Ser Ser Ser Ala Asp Pro Glu Gly			
225	230	235	240
His Phe Glu Thr Pro Ile Trp Ile Glu Arg Val Val Ile Ile Gly Ala			
245	250	255	
Gly Lys Pro Ala Ala Val Val Leu Gln Thr Lys Gly Ser Pro Glu Ser			
260	265	270	
Arg Leu Ser Phe Gln His Asp Pro Glu Thr Ser Val Leu Val Leu Arg			
275	280	285	
Lys Pro Gly Ile Asn Val Ala Ser Asp Trp Ser Ile His Leu Arg			
290	295	300	

<210> 10

<211> 160

<212> PRT

<213> Homo sapiens

<400> 10

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Met Asp Lys Leu Lys Lys Val Leu Ser Gly Gln Asp Thr Glu Asp Arg
 1 5 10 15
 Ser Gly Leu Ser Glu Val Val Glu Ala Ser Ser Leu Ser Trp Ser Thr
 20 25 30
 Arg Ile Lys Gly Phe Ile Ala Cys Phe Ala Ile Gly Ile Leu Cys Ser
 35 40 45
 Leu Leu Gly Thr Val Leu Leu Trp Val Pro Arg Lys Gly Leu His Leu
 50 55 60
 Phe Ala Val Phe Tyr Thr Phe Gly Asn Ile Ala Ser Ile Gly Ser Thr
 65 70 75 80
 Ile Phe Leu Met Gly Pro Val Lys Gln Leu Lys Arg Met Phe Glu Pro
 85 90 95
 Thr Arg Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe Ala Leu Thr
 100 105 110
 Leu Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala Leu Ile Phe
 115 120 125
 Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu Ser Phe Ile
 130 135 140
 Pro Phe Ala Arg Asp Ala Val Lys Lys Cys Phe Ala Val Cys Leu Ala
 145 150 155 160

<210> 11

<211> 1941

<212> DNA

<213> Homo sapiens

<400> 11

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 ctttgtgccg gggcgctctc ggcccggctg acggaggagg gcagcgggga cgccggtggc 120
 cgccgccgcc cgccagttga cccccggcga ttggcgcgcc agctgetget gctgettgg 180
 ctgetggagg ctccgctget gctgggggtc cgggcccagg cggcgggcca ggggccaggc 240
 cagggggccc ggcgggggca gcaaccgcgc ccgcccgcctc agcagcaaca gagcgggcag 300
 cagtacaacg gcgagcgggg catctccgtc ccggaccacg gctattgcc a gccatctcc 360
 atcccgtgt gcacggacat cgcgtacaac cagaccatca tgcccaacct gctgggccac 420
 acgaaccagg aggacgcggg cctggagggtg caccagttct accctctagt gaaagtgcag 480
 tgttccgctg agctcaagtt ctctctgtgc tccatgtacg cgcccggtg caccgtgcta 540

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gagcagggcg tgcggccctg ccgctccctg tgcgagcgcg cgcgccaggg ctgcgagggcg 600
 ctcatgaaca agttcggctt ccagtggcca gacacgctca agtgtgagaa gttcccgggtg 660
 cacggcgccg gcgagctgtg cgtgggccag aacacgtccg acaagggcac cccgacgccc 720
 tcgctgcttc cagagttctg gaccagcaac cctcagcacg gcggcggagg gcaccgtggc 780
 ggcttcccgg ggggcgcggc cgcgtcggag cgaggcaagt tctcctgccc gcgcgccctc 840
 aaggtgccct cctacctcaa ctaccacttc ctgggggaga aggactgcgg cgcaccttgt 900
 gagccgacca aggtgtatgg gctcatgtac ttccgggccg aggagctgcg cttctcgcg 960
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 tgttacacgg ccgtggccgt ggcctacatc gccggcttcc tcttgaaga ccgagtgtg 1140
 tgtaatgaca agttcgcga ggacggggca cgcactgtgg cgcagggcac caagaaggag 1200
 ggtgcacca tctcttcat gatgtcttac ttcttcagca tggccagctc catctggtg 1260
 gtgatctgt cgtcacctg gtctctggcg gctggcatga agtggggcca cggggccatc 1320
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 atcggcacgt cctttctgt ggccggcttt gtgtcgtct tccgcatccg caccatcatg 1560
 aagcagatg gcaccaagac cgagaagctg gagaagctca tggcgcgcac tggcgtcttc 1620
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 acggtcttca tgattaagta ccttatgacg ctgatcgtgg gcatcacgtc gggcttctgg 1860
 atctggctcg gcaagaccct caactcctgg aggaagttct acacgaggct caccaacagc 1920
 aaacaagggg agactacagt c 1941

<210> 12

<211> 1050

<212> DNA

<213> Homo sapiens

<400> 12

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 ccgacccggg ggctcattcg agcgacctcg gaccacaatg ccagcatgga ctttcagac 120
 cttccagctc tgtttggggc taccttgagc caggagggcc tccaggggtt ctttgtggag 180
 gctcaccag acaatgcctg cagccccatt gccccaccac cccagcccc ggtcaatggg 240
 tcagtcttta ttgcgtgct tcgaagattc gactgcaact ttgacctcaa ggtcctaaat 300

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gccagaagg ctggatatgg tgccgctgta gtacacaatg tgaattccaa tgaacttctg 360
aacatggtgt ggaatagtga ggaaatccag cagcagatct ggatcccgtc tgtattttatt 420
ggggagagaa gctccgagta cctgcgtgcc ctctttgtct acgagaaggg ggctcgggtg 480
cttctggttc cagacaatac cttccccttg ggctattacc tcatcccttt cacagggtatt 540
gtgggactgc tggttttggc catgggagca gtaatgatag ctcgttgtat ccagcacccg 600
aaacggctcc agcgggaatcg acttaccaaa gagcaactga aacagattec tacacatgac 660
tatcagaagg gagaccagta tgatgtctgt gccatttgcc tggatgaata tgaggatggg 720
gacaagctgc gggtaactcc ctgtgtcat gctaccaca gccgtgcgt ggacccctgg 780
ctcactcaga cccggaagac ctgccccatt tgcaagcagc ctgttcatcg gggctcctgg 840
gacgaagacc aagaggaaga aactcaaggg caagaggagg gtgatgaagg ggagccaagg 900
gaccaccctg cctcagaaag gaccccaact ttgggttcta gcccactct tcccacctcc 960
tttggttct tagccccagc tccccttgtt ttctctgggc cttcaacaga tccccactg 1020
tcccctccct cttcccctgt tatcctgggc 1050

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<210> 13

<211> 618

<212> DNA

<213> Homo sapiens

<400> 13

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tccctggctc tcttcaccac catcctgcac aatgtcttcc tgctctacta tgtggacacc 120
tttgtctcag tgtacaagat caacaaaatg gccttctggg tcggagagac agtgtttctc 180
ctctggaaca gcctcaatga cccctcttcc ggttggctca gtgaccggca gtctctcagc 240
tcccagcccc ggggaagaga tctaccctgg ctggtcttgg ttggccctc tggactgtgg 300
actgcaaaca ccctctgctg cttctggaag attcctttgc cccatccctg cttgagcccc 360
tcatcaccac caaccttgag aagtgggcac cccataccct ttggccatca gcccaacagg 420
ctaataaggg ggtggaaatt ggggcagagg aggagagtgt acccactggc caggcgccgg 480
gctctcctca agggctgtgg tgctggcccg ggtgcaggcc ctgggtgggc atgggcccgt 540
gtggtgcctg tegtctctgg cgttctgggt gccctgggac ccagctggcc tgcagttctt 600
gtgtgcctg tgctctca 618

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<210> 14

<211> 639

<212> DNA

<213> Homo sapiens

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<400> 14

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agctacaaca tcatcttctg gttggetgga gttgtcttcc ttggagtcgg gctgtgggca	120
tggagcgaaa aggggtgtgct gtccgacctc accaaagtga cccggatgca tggaaatcgac	180
cctgtggtgc tggctcctgat ggtgggctg gtgatgttca ccctgggggt cgccggtgc	240
gtgggggctc tgcgggagaa tatctgcttg ctcaacttta accagtgtg tggcgcatat	300
ggccctgaag actgggacct caacgtctac ttcaattgca gcggtgccag ctacagccga	360
gagaagtgcg gggccccctt ctctgtgtgc gtgccagatc ctgcgcaaaa agttgtgaac	420
acacagtgtg gatatgatgt caggattcag ctgaagagca agtgggatga gtccatcttc	480
acgaaaggct gcattccaggc gctggaaagc tggctccgc ggaacattta cattgtggct	540
ggcgtcttca tcgccatctc gctgttgag atatttgca tcttcctggc aaggacgctg	600
atctcagaca tcgaggcagt gaaggccgc catcacttc	639

<210> 15

<211> 1785

<212> DNA

<213> Homo sapiens

<400> 15

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aatgccgaac actcgtgtgc cactacctg ggcgtcttg agcggctgga ctacccccg	180
gccaggatgg ccctctggtg tgcacggac cacaatgtg acaacaccac agagatgtg	240
caggagtggc tggcggctgt gggcgatgac tatgtgtgtg tggctgtgag gcctgagggc	300
gagcccaggt tctaccaga tgaagagggt cccaagcact ggaccaaaga aaggcaccag	360
tttctgatgg agctgaagca ggaagccctc acctttgcca ggaactggg ggcgactat	420
atcctgtttg cagacacaga caacattctg accaacaatc agactctgcg gcttctcatg	480
gggcaggggc ttccagtgtt ggcaccaatg ctggactccc agacctacta ctccaacttc	540
tgggtgtgga tcacccccca gggctactac cgccgcacag ccgagtactt cccaccaa	600
aaccgcacgc gccggggctg ctccgctgtc cccatggctc actccacctt ccttgcatcc	660
ctgcgggctg aaggggcaga ccagcttgct ttctaccgc cacatcccaa ctacacttg	720
cctttcgacg acatcatcgt ctccgctat gcctgccagg ctgtgggggt ctccgtccac	780
gtgtgcaatg agcaccgtta tgggtacatg aatgtgccgg tgaaatccca ccaggggctg	840
gaagacgaga gggctcaact catccacctg atcttagaag cactagtgga cggccccgc	900
atgcaggcct cagctcatgt gactcggccc tctaagaggc ccagcaagat agggtttgac	960
gaggctcttg tcatcagcct ggtcgcagg cctgaccgtc gggaacgcat gctcgcctcg	1020

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ctctgggaga tggagatctc tgggaggggtg gtggacgctg tggatggctg gatgctcaac 1080
 agcagtgcc a tcaggaaacct cggcgtagac ctgctcccg gctaccagga cccttactcg 1140
 ggccgcactc tgaccaaggg cgaggtgggc tgttctctca gccattactc catctgggaa 1200
 gaggtggttg ccaggggcct ggcccgggtc ctggtgtttg aggatgacgt gcgctttgag 1260
 agcaacttca gggggcggct ggagcggctg atggaggatg tggaggcaga gaaactgtct 1320
 tgggacctga tctacctcg acggaagcag gtgaacctg agaaggagac ggccgtggag 1380
 gggtgcccgg gcctggtggt ggctgggtac tctactgga cgctggccta tgcctgcgt 1440
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 gagtctctgc ccatcatgtt cgaccagcac cccaacgagc agtacaaggc acacttctgg 1560
 ccacgggacc tgggtggcctt ctccgcccag cccctgctcg ctgcccctac ccactatgcc 1620
 ggggacgccg agtggctcag tgacacggag acatcctctc catgggatga tgacagcggc 1680
 cgctcatca gctggagcgg ctcccaaaag accctgcgca gccccgcct ggacctgact 1740
 ggcagcagcg ggcacagcct ccaaccccag ccccgagatg agctc 1785

<210> 16

<211> 792

<212> DNA

<213> Homo sapiens

<400> 16

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 gagactggct gctgcacct a tactatgag ctctggtggt tctggctgct ctggactgtc 180
 ctcacctct ttagctgctg ttgcgccttc cgccacccgac gagctaaact caggctgcaa 240
 caacagcagc ggcagcgtga aatcaacttg ttggcctatc atggggcatg ccattggggct 300
 ggtcctttcc ctaccgggtc actgcttgac cttcgcttcc tcagcacctt caagccccca 360
 gcctacgagg atgtggttca ccgccaggc acaccacccc ccccttatac tgtggcccca 420
 ggccgcccct tgaactgctc cagtgaacaa acctgctgtt cctcctcatc cagctgcct 480
 gccactttg aaggaacaaa tgtggaagggt gtttcctccc accagagtgc cccccccat 540
 caggaggggt agcccggggc aggggtgacc cctgcctcca cccccctc ctgccgtat 600
 cgccgtttaa ctgggactc cggatttgag ctctgccctt gtctgcctc cggtaggggt 660
 gagccagtca aggaggtgag ggttagtgcc acctgccag atctggagga ctactccccg 720
 tgtgcactac cccagagtc tgtaccgag atctttccca tggggctgtc ttccagtga 780
 ggggacatcc ca 792

<210> 17

20/233

<211> 1029

<212> DNA

<213> Homo sapiens

<400> 17

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atgcagcccc cgcccccggg cccgctgggc gactgcctgc gggactggga ggatctacag    60
caggacttcc agaacatcca ggagacccat cggctctacc gcctgaagct ggaggagctg    120
accaaacttc agaacaattg caccagctcc atcacgcggc agaagaagcg gctccaggag    180
ctggccctcg cctgaagaa atgcaaacc tccctcccag cagaggccga gggggccgca    240
caggagctgg agaaccagat gaaagagcgc caaggcctct tctttgacat ggaggcctat    300
ttgcctaaga agaatggatt gtacctgagc ctggtttotgg ggaacgtcaa cgtcacgctc    360
ctgagcaagc aggetaagtt tgectacaag gacgagtatg agaagttcaa gctctacctc    420
accatcatcc tcctcctcat ctcttccact tgccgcttcc tgcctcaact cagggtgaca    480
gatgtgcctt tcaacttcct gctggtotgg tactactgca cctgacctat ccgggagagc    540
atctcatca acaacggctc ccggatcaaa ggctggtggg tgttccatca ctacgtgtcc    600
accttcctgt cgggagtcac gctgacgtgg ccgacggctc tcatgtacca gaaattccgg    660
aaccaattcc tctccttttc catgtaccag agcttcgtgc agtttctcca gtactactac    720
cagagcggct gcctctaccg cctgcgggcg ctgggcgagc ggcacacctt ggacctcact    780
gtggagggct tccagtcctg gatgtggcgg ggctcacctc tctgctgcc ttttcttttc    840
tttgacact tctggcagct ttttaacgcg ctgacgttgt tcaacctggc ccaggacctt    900
cagtgaagg agtggcaggt gcttatgtgc ggctttccct tctcctcct tttcctcgge    960
aatttcttca ccacctgag ggttgtgcac cacaagtttc acagtcagcg gcacgggagc   1020
aagaaggat                                     1029

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<210> 18

<211> 732

<212> DNA

<213> Homo sapiens

<400> 18

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gccgtgctga ctccaagag caaccgcaag atggagagca agaaacggga gctcttcagc    180
cagataaagg ggcttacagg agctccggg aaagtggccc tactggagct gggctgcgga    240
accggagcca actttcagtt ctaccaccg ggctgcaggg tcacctgctt agacccaaat    300
ccccactttg agaagttcct gacaaagagc atggctgaga acaggcacct ccaatatgag    360
cggttttggt tggctcctgg agaggacatg agacagctgg ctgatggctc catggatgtg    420

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gtggtctgca ctctggtgct gtgctctgtg cagagcccaa ggaaggctcct gcaggaggtc 480
 cggagagtagc tgagaccggg aggtgtgtctc tttttctggg agcatgtggc agaaccatat 540
 ggaagctggg ccttcattgtg gcagcaagtt ttcgagccca cctggaaaca cattggggat 600
 ggctgtgtcc tcaccagaga gacctggaag gatcttgaga acgcccagtt ctccgaaatc 660
 caaatggaac gacagccccc tcccttgaag tggctacctg ttgggcccga catcatggga 720
 aaggctgtca aa 732

<210> 19

<211> 909

<212> DNA

<213> Homo sapiens

<400> 19

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 ctctacgcgc tgggtacagct cggccagcca tgtgactgcc ttcctcccct gcgggcagca 120
 gccgagcagc tacggcagaa ggatctgagg atttcccagc tgcaagcggg actccgacgg 180
 ccccccctg cccctgcccga gcccctgaa cccgaggccc tgcctactat ctatgttgtt 240
 acccccacct atgccaggcc cctgtgggtg cagtaccctc aggatgtgac taccttcaat 300
 atagatgac agtaacttgc tggggatgag ttgtgtgttc accctgtatc agaactctgga 360
 gcccatggtg tccaggtcta tctgcctggc caaggggagg tgtggtatga cattcaaagc 420
 taccagaagc atcatggtcc ccagaccctg tacctgcctg taactctaaag cagtatccct 480
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 tgtatgaagg atgaccccat cactctcttt gttgcactta gccctcaggg tacagctcaa 600
 ggagagctct ttctggatga tgggcacacg ttcaactatc agactcggca agagttcctg 660
 ctgcgtcgat tctcattctc tggcaacacc cttgtctcca gtcagcaga ccctgaagga 720
 cactttgaga caccaatctg gattgagcgg gtggtgataa taggggctgg aaagccagca 780
 gctgtggtac tccagacaaa aggatctcca gaaagccgcc tgtccttcca gcataccct 840
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<211> 480

<212> DNA

<213> Homo sapiens

<400> 20

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 ggactacacc tcttcgcagt gttttatacc tttggttaata tcgcatcaat tgggagtacc 240
 atcttcctca tgggaccagt gaaacagctg aagcgaatgt ttgagcctac tcgtttgatt 300
 gcaactatca tgggtgctgt gtgttttgca cttaccctgt gttctgcctt ttggtggcat 360
 aacaagggac ttgcacttat cttctgcatt ttgcagctct tggcattgac gtggtacagc 420
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<210> 21

<211> 4485

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<213> Homo sapiens

<220>

<221> CDS

<222> (189)...(2132)

<400> 21

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 gggagccgcc gccggccgtg cccctggcag cccagcggga gcggcgccaa gagaggagcc 180
 gagaaagt atg gct gag gag gag gcg cct aag aag tcc cgg gcc gcc ggc 230
 Met Ala Glu Glu Glu Ala Pro Lys Lys Ser Arg Ala Ala Gly
 1 5 10
 ggt ggc gcg agc tgg gaa ctt tgt gcc ggg gcg ctc tog gcc cgg ctg 278
 Gly Gly Ala Ser Trp Glu Leu Cys Ala Gly Ala Leu Ser Ala Arg Leu
 15 20 25 30
 acg gag gag ggc agc ggg gac gcc ggt ggc cgc cgc cgc ccg cca gtt 326
 Thr Glu Glu Gly Ser Gly Asp Ala Gly Gly Arg Arg Arg Pro Pro Val
 35 40 45
 gac ccc cgg cga ttg gcg cgc cag ctg ctg ctg ctg ctt tgg ctg ctg 374
 Asp Pro Arg Arg Leu Ala Arg Gln Leu Leu Leu Leu Trp Leu Leu
 50 55 60
 gag gct ccg ctg ctg ctg ggg gtc cgg gcc cag gcg gcg ggc cag ggg 422
 Glu Ala Pro Leu Leu Leu Gly Val Arg Ala Gln Ala Ala Gly Gln Gly
 65 70 75
 cca ggc cag ggg ccc ggg ccg ggg cag caa ccg ccg ccg ccg cct cag 470

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Pro Gly Gln Gly Pro Gly Pro Gly Gln Gln Pro Pro Pro Pro Pro Gln	
80 85 90	
cag caa cag agc ggg cag cag tac aac ggc gag cgg ggc atc tcc gtc	518
Gln Gln Gln Ser Gly Gln Gln Tyr Asn Gly Glu Arg Gly Ile Ser Val	
95 100 105 110	
ccg gac cac ggc tat tgc cag ccc atc tcc atc ccg ctg tgc acg gac	566
Pro Asp His Gly Tyr Cys Gln Pro Ile Ser Ile Pro Leu Cys Thr Asp	
115 120 125	
atc gcg tac aac cag acc atc atg ccc aac ctg ctg ggc cac acg aac	614
Ile Ala Tyr Asn Gln Thr Ile Met Pro Asn Leu Leu Gly His Thr Asn	
130 135 140	
cag gag gac gcg ggc ctg gag gtg cac cag ttc tac cct cta gtg aaa	662
Gln Glu Asp Ala Gly Leu Glu Val His Gln Phe Tyr Pro Leu Val Lys	
145 150 155	
gtg cag tgt tcc gct gag ctc aag ttc ttc ctg tgc tcc atg tac gcg	710
Val Gln Cys Ser Ala Glu Leu Lys Phe Phe Leu Cys Ser Met Tyr Ala	
160 165 170	
ccc gtg tgc acc gtg cta gag cag gcg ctg ccg ccc tgc cgc tcc ctg	758
Pro Val Cys Thr Val Leu Glu Gln Ala Leu Pro Pro Cys Arg Ser Leu	
175 180 185 190	
tgc gag cgc gcg cgc cag ggc tgc gag gcg ctc atg aac aag ttc ggc	806
Cys Glu Arg Ala Arg Gln Gly Cys Glu Ala Leu Met Asn Lys Phe Gly	
195 200 205	
ttc cag tgg cca gac acg ctc aag tgt gag aag ttc ccg gtg cac ggc	854
Phe Gln Trp Pro Asp Thr Leu Lys Cys Glu Lys Phe Pro Val His Gly	
210 215 220	
gcc ggc gag ctg tgc gtg ggc cag aac acg tcc gac aag ggc acc ccg	902
Ala Gly Glu Leu Cys Val Gly Gln Asn Thr Ser Asp Lys Gly Thr Pro	
225 230 235	
acg ccc tcg ctg ctt cca gag ttc tgg acc agc aac cct cag cac ggc	950
Thr Pro Ser Leu Leu Pro Glu Phe Trp Thr Ser Asn Pro Gln His Gly	
240 245 250	
ggc gga ggg cac cgt ggc ggc ttc ccg ggg ggc gcc ggc gcg tcg gag	998
Gly Gly Gly His Arg Gly Gly Phe Pro Gly Gly Ala Gly Ala Ser Glu	
255 260 265 270	

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cga ggc aag ttc tcc tgc ccg cgc gcc ctc aag gtg ccc tcc tac ctc	1046
Arg Gly Lys Phe Ser Cys Pro Arg Ala Leu Lys Val Pro Ser Tyr Leu	
275 280 285	
aac tac cac ttc ctg ggg gag aag gac tgc ggc gca cct tgt gag ccg	1094
Asn Tyr His Phe Leu Gly Glu Lys Asp Cys Gly Ala Pro Cys Glu Pro	
290 295 300	
acc aag gtg tat ggg ctc atg tac ttc ggg ccc gag gag ctg cgc ttc	1142
Thr Lys Val Tyr Gly Leu Met Tyr Phe Gly Pro Glu Glu Leu Arg Phe	
305 310 315	
tcg cgc acc tgg att ggc att tgg tca gtg ctg tgc tgc gcc tcc acg	1190
Ser Arg Thr Trp Ile Gly Ile Trp Ser Val Leu Cys Cys Ala Ser Thr	
320 325 330	
ctc ttc acg gtg ctt acg tac ctg gtg gac atg cgg cgc ttc agc tac	1238
Leu Phe Thr Val Leu Thr Tyr Leu Val Asp Met Arg Arg Phe Ser Tyr	
335 340 345 350	
ccg gag cgg ccc atc atc ttc ttg tcc ggc tgt tac acg gcc gtg gcc	1286
Pro Glu Arg Pro Ile Ile Phe Leu Ser Gly Cys Tyr Thr Ala Val Ala	
355 360 365	
gtg gcc tac atc gcc ggc ttc ctc ctg gaa gac cga gtg gtg tgt aat	1334
Val Ala Tyr Ile Ala Gly Phe Leu Leu Glu Asp Arg Val Val Cys Asn	
370 375 380	
gac aag ttc gcc gag gac ggg gca cgc act gtg gcg cag ggc acc aag	1382
Asp Lys Phe Ala Glu Asp Gly Ala Arg Thr Val Ala Gln Gly Thr Lys	
385 390 395	
aag gag ggc tgc acc atc ctc ttc atg atg ctc tac ttc ttc agc atg	1430
Lys Glu Gly Cys Thr Ile Leu Phe Met Met Leu Tyr Phe Phe Ser Met	
400 405 410	
gcc agc tcc atc tgg tgg gtg atc ctg tcg ctc acc tgg ttc ctg gcg	1478
Ala Ser Ser Ile Trp Trp Val Ile Leu Ser Leu Thr Trp Phe Leu Ala	
415 420 425 430	
gct ggc atg aag tgg ggc cac gag gcc atc gaa gcc aac tca cag tat	1526
Ala Gly Met Lys Trp Gly His Glu Ala Ile Glu Ala Asn Ser Gln Tyr	
435 440 445	
ttt cac ctg gcc gcc tgg gct gtg ccg gcc atc aag acc atc acc atc	1574
Phe His Leu Ala Ala Trp Ala Val Pro Ala Ile Lys Thr Ile Thr Ile	

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450	455	460	
ctg gcg ctg ggc cag gtg gac ggc gat gtg ctg agc gga gtg tgc ttc			1622
Leu Ala Leu Gly Gln Val Asp Gly Asp Val Leu Ser Gly Val Cys Phe			
465	470	475	
gtg ggg ctt aac aac gtg gac gcg ctg cgt ggc ttc gtg ctg gcg ccc			1670
Val Gly Leu Asn Asn Val Asp Ala Leu Arg Gly Phe Val Leu Ala Pro			
480	485	490	
ctc ttc gtg tac ctg ttt atc ggc acg tcc ttt ctg ctg gcc ggc ttt			1718
Leu Phe Val Tyr Leu Phe Ile Gly Thr Ser Phe Leu Leu Ala Gly Phe			
495	500	505	510
gtg teg ctc ttc cgc atc cgc acc atc atg aag cac gat ggc acc aag			1766
Val Ser Leu Phe Arg Ile Arg Thr Ile Met Lys His Asp Gly Thr Lys			
515	520	525	
acc gag aag ctg gag aag ctc atg gtg cgc att ggc gtc ttc agc gtg			1814
Thr Glu Lys Leu Glu Lys Leu Met Val Arg Ile Gly Val Phe Ser Val			
530	535	540	
ctg tac act gtg cca gcc acc atc gtc atc gcc tgc tac ttc tac gag			1862
Leu Tyr Thr Val Pro Ala Thr Ile Val Ile Ala Cys Tyr Phe Tyr Glu			
545	550	555	
cag gcc ttc cgg gac cag tgg gaa cgc agc tgg gtg gcc cag agc tgc			1910
Gln Ala Phe Arg Asp Gln Trp Glu Arg Ser Trp Val Ala Gln Ser Cys			
560	565	570	
aag agc tac gct atc ccc tgc cct cac ctc cag gcg ggc gga ggc gcc			1958
Lys Ser Tyr Ala Ile Pro Cys Pro His Leu Gln Ala Gly Gly Gly Ala			
575	580	585	590
ccg ccg cac ccg ccc atg agc ccg gac ttc acg gtc ttc atg att aag			2006
Pro Pro His Pro Pro Met Ser Pro Asp Phe Thr Val Phe Met Ile Lys			
595	600	605	
tac ctt atg acg ctg atc gtg ggc atc acg teg ggc ttc tgg atc tgg			2054
Tyr Leu Met Thr Leu Ile Val Gly Ile Thr Ser Gly Phe Trp Ile Trp			
610	615	620	
tcc ggc aag acc ctc aac tcc tgg agg aag ttc tac acg agg ctc acc			2102
Ser Gly Lys Thr Leu Asn Ser Trp Arg Lys Phe Tyr Thr Arg Leu Thr			
625	630	635	
aac agc aaa caa ggg gag act aca gtc tgagaccgg ggctcagccc a			2150

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Asn Ser Lys Gln Gly Glu Thr Thr Val

640

645

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gagggaggat	ggacagacct	ottgccctca	cactctggta	ccaggactgt	tcgcttttat	2390
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cacgcgtttt	tctttttcaa	aagtttttaa	ttatttaggg	cggtttaacc	atttgaggct	2510
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cagaaatgtg	tcaaatgtaa	atctttcaaa	gccattttaa	aatattcact	ttagttctct	3770
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aaagttttgt	acaaaattat	atggattttg	tgcttgaaaa	taatagagct	tgagctgtct	4070
gaactatTTT	acattttatg	gtgtctcata	gccaatcccc	cagtgtaaaa	attcaggaat	4130

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tcaatgaaaa aagtctaccc ttaaaccctc agatcagtct ttccaaagaa ttactctgtt 4190
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 aaaaatagaag ttgcaaatt atttctttac tcaaagagga ttaaagaga actctaattt 4310
 taatattaaa gctttctttt ctttcagggg ataaatttac atgacttttt atattatgga 4370
 ggtttatttt taaatcatca cttttctcat attttttaga ggtattgtct tatctcttcc 4430
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<213> Homo sapiens

<220>

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 agctgggaag tgggacctgg ggggtggttg acccctggga tcctaaagga ggggcagggg 180
 ggggcagagaa ctccgcttct gctccttget accaggacgc ggggcctcct cagcctcttt 240
 cctcccgtg cc atg cac cct gca gcc ttc ccg ctt cct gtg gtt gtg gcc 291

Met His Pro Ala Ala Phe Pro Leu Pro Val Val Val Ala

1

5

10

got gtg ctg tgg gga gcg gcc ccg acc cgg ggg ctc att cga gcg acc 339
 Ala Val Leu Trp Gly Ala Ala Pro Thr Arg Gly Leu Ile Arg Ala Thr

15

20

25

tcg gac cac aat gcc agc atg gac ttt gca gac ctt cca got ctg ttt 387
 Ser Asp His Asn Ala Ser Met Asp Phe Ala Asp Leu Pro Ala Leu Phe

30

35

40

45

ggg got acc ttg agc cag gag ggc ctc cag ggg ttc ctt gtg gag got 435
 Gly Ala Thr Leu Ser Gln Glu Gly Leu Gln Gly Phe Leu Val Glu Ala

50

55

60

cac cca gac aat gcc tgc agc ccc att gcc cca cca ccc cca gcc ccg 483
 His Pro Asp Asn Ala Cys Ser Pro Ile Ala Pro Pro Pro Pro Ala Pro

65

70

75

gtc aat ggg tca gtc ttt att gcg ctg ctt cga aga ttc gac tgc aac 531

28/233

Val Asn Gly Ser Val Phe Ile Ala Leu Leu Arg Arg Phe Asp Cys Asn	
80 85 90	
ttt gac ctc aag gtc cta aat gcc cag aag gct gga tat ggt gcc gct	579
Phe Asp Leu Lys Val Leu Asn Ala Gln Lys Ala Gly Tyr Gly Ala Ala	
95 100 105	
gta gta cac aat gtg aat tcc aat gaa ctt ctg aac atg gtg tgg aat	627
Val Val His Asn Val Asn Ser Asn Glu Leu Leu Asn Met Val Trp Asn	
110 115 120 125	
agt gag gaa atc cag cag cag atc tgg atc ccg tct gta ttt att ggg	675
Ser Glu Glu Ile Gln Gln Gln Ile Trp Ile Pro Ser Val Phe Ile Gly	
130 135 140	
gag aga agc tcc gag tac ctg cgt gcc ctc ttt gtc tac gag aag ggg	723
Glu Arg Ser Ser Glu Tyr Leu Arg Ala Leu Phe Val Tyr Glu Lys Gly	
145 150 155	
gct cgg gtg ctt ctg gtt cca gac aat acc ttc ccc ttg ggc tat tac	771
Ala Arg Val Leu Leu Val Pro Asp Asn Thr Phe Pro Leu Gly Tyr Tyr	
160 165 170	
ctc atc cct ttc aca ggg att gtg gga ctg ctg gtt ttg gcc atg gga	819
Leu Ile Pro Phe Thr Gly Ile Val Gly Leu Leu Val Leu Ala Met Gly	
175 180 185	
gca gta atg ata gct cgt tgt atc cag cac cgg aaa cgg ctc cag cgg	867
Ala Val Met Ile Ala Arg Cys Ile Gln His Arg Lys Arg Leu Gln Arg	
190 195 200 205	
aat cga ctt acc aaa gag caa ctg aaa cag att cct aca cat gac tat	915
Asn Arg Leu Thr Lys Glu Gln Leu Lys Gln Ile Pro Thr His Asp Tyr	
210 215 220	
cag aag gga gac cag tat gat gtc tgt gcc att tgc ctg gat gaa tat	963
Gln Lys Gly Asp Gln Tyr Asp Val Cys Ala Ile Cys Leu Asp Glu Tyr	
225 230 235	
gag gat ggg gac aag ctg cgg gta ctc ccc tgt gct cat gcc tac cac	1011
Glu Asp Gly Asp Lys Leu Arg Val Leu Pro Cys Ala His Ala Tyr His	
240 245 250	
agc cgc tgc gtg gac ccc tgg ctc act cag acc cgg aag acc tgc ccc	1059
Ser Arg Cys Val Asp Pro Trp Leu Thr Gln Thr Arg Lys Thr Cys Pro	
255 260 265	

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att tgc aag cag cct gtt cat cgg ggt cct ggg gac gaa gac caa gag      1107
Ile Cys Lys Gln Pro Val His Arg Gly Pro Gly Asp Glu Asp Gln Glu
270                275                280                285
gaa gaa act caa ggg caa gag gag ggt gat gaa ggg gag cca agg gac      1155
Glu Glu Thr Gln Gly Gln Glu Glu Gly Asp Glu Gly Glu Pro Arg Asp
                290                295                300
cac cct gcc tca gaa agg acc cca ctt ttg ggt tct agc ccc act ctt      1203
His Pro Ala Ser Glu Arg Thr Pro Leu Leu Gly Ser Ser Pro Thr Leu
                305                310                315
ccc acc tcc ttt ggt tcc tta gcc cca gct ccc ctt gtt ttt cct ggg      1251
Pro Thr Ser Phe Gly Ser Leu Ala Pro Ala Pro Leu Val Phe Pro Gly
                320                325                330
cct tca aca gat ccc cca ctg tcc cct ccc tct tcc cct gtt atc ctg      1299
Pro Ser Thr Asp Pro Pro Leu Ser Pro Pro Ser Ser Pro Val Ile Leu
                335                340                345
gtc taataacccc ccacacatac acctctggtg acctatttgc acagaccg      1350
Val
350
tcgttcttccc tccagtcttc tgagggatag gggacattcc atcccaagct tctcccttac      1410
ccacacctat ccttttgagg ggctttgggg tggggctggg gcaagcagag ggactgggtc      1470
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<211> 3059

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<220>

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<222> (230)...(850)

<400> 23

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acaaggatat ttacctgctc ctacctgat ctagggaaga gcatgggaag accgcctgtg      180
gcatgagacc ctcccgggtg ctccctgggc taaggctggg gctgcagcc atg ggg ctg      238
Met Gly Leu

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1

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 Gly Gln Pro Gln Ala Trp Leu Leu Gly Leu Pro Thr Ala Val Val Tyr
 5 10 15

ggc tcc ctg gct ctc ttc acc acc atc ctg cac aat gtc ttc ctg ctc 334
 Gly Ser Leu Ala Leu Phe Thr Thr Ile Leu His Asn Val Phe Leu Leu
 20 25 30 35

tac tat gtg gac acc ttt gtc tca gtg tac aag atc aac aaa atg gcc 382
 Tyr Tyr Val Asp Thr Phe Val Ser Val Tyr Lys Ile Asn Lys Met Ala
 40 45 50

ttc tgg gtc gga gag aca gtg ttt ctc ctc tgg aac agc ctc aat gac 430
 Phe Trp Val Gly Glu Thr Val Phe Leu Leu Trp Asn Ser Leu Asn Asp
 55 60 65

ccc ctc ttc ggt tgg ctc agt gac cgg cag ttc ctc agc tcc cag ccc 478
 Pro Leu Phe Gly Trp Leu Ser Asp Arg Gln Phe Leu Ser Ser Gln Pro
 70 75 80

cgg gga aga gat cta ccc tgg ctt ggc ttg gtt ggc ccc tct gga ctg 526
 Arg Gly Arg Asp Leu Pro Trp Leu Gly Leu Val Gly Pro Ser Gly Leu
 85 90 95

tgg act gca aac acc ctc tgc tgc ttc tgg aag att cct ttg ccc cat 574
 Trp Thr Ala Asn Thr Leu Cys Cys Phe Trp Lys Ile Pro Leu Pro His
 100 105 110 115

ccc tgc ttg agc ccg tca tca ccc cca acc ttg aga agt ggg cat ccc 622
 Pro Cys Leu Ser Pro Ser Ser Pro Pro Thr Leu Arg Ser Gly His Pro
 120 125 130

ata ccc ttt ggc cat cag ccc aac agg cta ata agg ggg tgg aaa ttg 670
 Ile Pro Phe Gly His Gln Pro Asn Arg Leu Ile Arg Gly Trp Lys Leu
 135 140 145

ggg cag agg agg aga gtg tac cca ctg gtc agg cgc cgg gct ctc ctc 718
 Gly Gln Arg Arg Arg Val Tyr Pro Leu Val Arg Arg Arg Ala Leu Leu
 150 155 160

aag ggc tgt ggt gct ggc ccg ggt gca ggc cct ggg ctg gca tgg gcc 766
 Lys Gly Cys Gly Ala Gly Pro Gly Ala Gly Pro Gly Leu Ala Trp Ala
 165 170 175

gct gct ggc gct gtc gtt cct ggc gtt ctg ggt gcc ctg ggc ccc agc 814

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190	195
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Trp Pro Ala Val Leu Ala Val Pro Val Pro Leu	
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cgcacccacc tcaacttcta ctgtccctc ttcagcggcg ccggtccct ctctgtcttt	980
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ggcgtgagcc actgtggcca acctaatctt tgtattattt agtagagaca gggtttcacc	2420
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aaagtgtgg gaatacaggc atgagccacc gcactcggcc aggagctagt tttaccagca	2540
tcctgtctca ctgccttctc ctagtgcagc ctggaagaca tggcagcggg tagctcctgg	2600
ggctgagcca gaagcatcac tgcagtgaat gtctctgctt acctgtctgg ctacagcttg	2660

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gcaagggctg ggccatatgt gctcagggac gtgcttctct tgtaaggcag gaggatagaa 2720
 gaggaccaag aagggagggg gctgccctgt ggtgcacaca ggctgccat ggggcgtggg 2780
 agcccatccc gctgcctgac tggagctggc cgtgtgtgtg gactcaggaa ccacttttaa 2840
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<210> 24

<211> 2367

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (69)...(710)

<400> 24

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 ctcagaag atg cac tat tat aga tac tct aac gcc aag gtc agc tgc tgg 110
 Met His Tyr Tyr Arg Tyr Ser Asn Ala Lys Val Ser Cys Trp
 1 5 10
 tac aag tac ctc ctt ttc agc tac aac atc atc ttc tgg ttg gct gga 158
 Tyr Lys Tyr Leu Leu Phe Ser Tyr Asn Ile Ile Phe Trp Leu Ala Gly
 15 20 25 30
 gtt gtc ttc ctt gga gtc ggg ctg tgg gca tgg agc gaa aag ggt gtg 206
 Val Val Phe Leu Gly Val Gly Leu Trp Ala Trp Ser Glu Lys Gly Val
 35 40 45
 ctg tcc gac ctc acc aaa gtg acc cgg atg cat gga atc gac cct gtg 254
 Leu Ser Asp Leu Thr Lys Val Thr Arg Met His Gly Ile Asp Pro Val
 50 55 60
 gtg ctg gtc ctg atg gtg ggc gtg gtg atg ttc acc ctg ggg ttc gcc 302
 Val Leu Val Leu Met Val Gly Val Val Met Phe Thr Leu Gly Phe Ala
 65 70 75
 ggc tgc gtg ggg gct ctg cgg gag aat atc tgc ttg ctc aac ttt aac 350
 Gly Cys Val Gly Ala Leu Arg Glu Asn Ile Cys Leu Leu Asn Phe Asn
 80 85 90

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cag tgc tgt ggc gca tat ggc cct gaa gac tgg gac ctc aac gtc tac 398
 Gln Cys Cys Gly Ala Tyr Gly Pro Glu Asp Trp Asp Leu Asn Val Tyr
 95 100 105 110
 ttc aat tgc agc ggt gcc agc tac agc cga gag aag tgc ggg gtc ccc 446
 Phe Asn Cys Ser Gly Ala Ser Tyr Ser Arg Glu Lys Cys Gly Val Pro
 115 120 125
 ttc tcc tgc tgc gtg cca gat cct gcg caa aaa gtt gtg aac aca cag 494
 Phe Ser Cys Cys Val Pro Asp Pro Ala Gln Lys Val Val Asn Thr Gln
 130 135 140
 tgt gga tat gat gtc agg att cag ctg aag agc aag tgg gat gag tcc 542
 Cys Gly Tyr Asp Val Arg Ile Gln Leu Lys Ser Lys Trp Asp Glu Ser
 145 150 155
 atc ttc acg aaa ggc tgc atc cag gcg ctg gaa agc tgg ctc ccg cgg 590
 Ile Phe Thr Lys Gly Cys Ile Gln Ala Leu Glu Ser Trp Leu Pro Arg
 160 165 170
 aac att tac att gtg gct ggc gtc ttc atc gcc atc tcg ctg ttg cag 638
 Asn Ile Tyr Ile Val Ala Gly Val Phe Ile Ala Ile Ser Leu Leu Gln
 175 180 185 190
 ata ttt ggc atc ttc ctg gca agg acg ctg atc tca gac atc gag gca 686
 Ile Phe Gly Ile Phe Leu Ala Arg Thr Leu Ile Ser Asp Ile Glu Ala
 195 200 205
 gtg aag gcc ggc cat cac ttc tgaggagcag agttgaggga gccgagctga gcc 740
 Val Lys Ala Gly His His Phe
 210
 acgctgggag gccagagcct ttctctgccca tcagccctac gtccagaggg agaggagccg 800
 acacccccag agccagtgcc ccatcttaag catcagcgtg acgtgacctc totgtttctg 860
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 gcctctgagt gccagcgag totgtctggga catgcacata tcaggggttg tttgcaggat 1280
 cctcagccat gttcaagtga agtaagcctg agccagtgcg tggactggtg ccacgggagt 1340
 gcttgtcca ctgtccccct gtgtccacca gctattctcc tggcgccgga actgcctctg 1400

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gtottgatag cattaagccc tgatggcgcc ggtggcgcggt tgggcatggt tottcaactga 1460
gagccgggtc tcctttttctt aaagtgtgta aatagtttat ttataggggt aagaatgttc 1520
tcacaccatt tcaacttctc ttctctctct ccagcattct cctctgagca gccttagata 1580
gtgtccatgg ctggagccga ccctttgagt cccttgagt gtottaagaa ccagcccaca 1640
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tgccatttgc ctctccccgg agacagcgtt tcttctgcaa ccacaccccg tgcttagcca 1940
caaccccagg ctgcagctgc tcagaagctc caggcatttt gtttctggtg accgccccta 2000
atgggatata ggtgatcact ggtccaccct tcctgtcagg gcttttctgg ggtgctctt 2060
ggaaatgaag tcttaagtac tgaataactc ccctggggat agctggggca tttgtotagc 2120
tgggctactt tctaacactt tgccatagct cagaccactt ctcatcggtc agggatggac 2180
tgcaacctta atttacttgc cggagtgtac attctagtgt ggtgtatact ggtggctgtt 2240
gatgatgatt tttttttttt ttttttacac aattctctgt agactaggag aagaatgctt 2300
gtgtttttcg gaagtgtgat gcttctcttt gactgccaaa ctcttttatg gaatatatct 2360
ttatatatt 2367

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<210> 25

<211> 2355

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (20)...(1807)

<400> 25

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Met Arg Ala Ala Arg Ala Ala Pro Leu Leu Gln
1 5 10
ctg ctg ctc ctg ctg ggg ccg tgg ctg gag gct gcg gcc gtt gcg gag 100
Leu Leu Leu Leu Leu Gly Pro Trp Leu Glu Ala Ala Gly Val Ala Glu
15 20 25
tcg ccg ctg ccc gcc gtg gtc ctt gcc atc ctg gcc cgc aat gcc gaa 148
Ser Pro Leu Pro Ala Val Val Leu Ala Ile Leu Ala Arg Asn Ala Glu
30 35 40

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cac tgc ctg ccc cac tac ctg ggc gct ctg gag cgg ctg gac tac ccc	196
His Ser Leu Pro His Tyr Leu Gly Ala Leu Glu Arg Leu Asp Tyr Pro	
45 50 55	
cgg gcc agg atg gcc ctc tgg tgt gcc acg gac cac aat gtg gac aac	244
Arg Ala Arg Met Ala Leu Trp Cys Ala Thr Asp His Asn Val Asp Asn	
60 65 70 75	
acc aca gag atg ctg cag gag tgg ctg gcg gct gtg ggc gat gac tat	292
Thr Thr Glu Met Leu Gln Glu Trp Leu Ala Ala Val Gly Asp Asp Tyr	
80 85 90	
gct gct gtg gtc tgg agg cct gag ggc gag ccc agg ttc tac cca gat	340
Ala Ala Val Val Trp Arg Pro Glu Gly Glu Pro Arg Phe Tyr Pro Asp	
95 100 105	
gaa gag ggt ccc aag cac tgg acc aaa gaa agg cac cag ttt ctg atg	388
Glu Glu Gly Pro Lys His Trp Thr Lys Glu Arg His Gln Phe Leu Met	
110 115 120	
gag ctg aag cag gaa gcc ctc acc ttt gcc agg aac tgg ggg gcc gac	436
Glu Leu Lys Gln Glu Ala Leu Thr Phe Ala Arg Asn Trp Gly Ala Asp	
125 130 135	
tat atc ctg ttt gca gac aca gac aac att ctg acc aac aat cag act	484
Tyr Ile Leu Phe Ala Asp Thr Asp Asn Ile Leu Thr Asn Asn Gln Thr	
140 145 150 155	
ctg cgg ctt ctc atg ggg cag ggg ctt cca gtg gtg gcc cca atg ctg	532
Leu Arg Leu Leu Met Gly Gln Gly Leu Pro Val Val Ala Pro Met Leu	
160 165 170	
gac tcc cag acc tac tac tcc aac ttc tgg tgt ggg atc acc ccc cag	580
Asp Ser Gln Thr Tyr Tyr Ser Asn Phe Trp Cys Gly Ile Thr Pro Gln	
175 180 185	
ggc tac tac cgc cgc aca gcc gag tac ttc ccc acc aag aac cgc cag	628
Gly Tyr Tyr Arg Arg Thr Ala Glu Tyr Phe Pro Thr Lys Asn Arg Gln	
190 195 200	
cgc cgg ggc tgc ttc cgt gtc ccc atg gtc cac tcc acc ttc ctt gca	676
Arg Arg Gly Cys Phe Arg Val Pro Met Val His Ser Thr Phe Leu Ala	
205 210 215	
tcc ctg cgg gct gaa ggg gca gac cag ctt gct ttc tac ccg cca cat	724
Ser Leu Arg Ala Glu Gly Ala Asp Gln Leu Ala Phe Tyr Pro Pro His	

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220	225	230	235	
ccc aac tac act tgg cct ttc gac gac atc atc gtc ttc gcc tat gcc				772
Pro Asn Tyr Thr Trp Pro Phe Asp Asp Ile Ile Val Phe Ala Tyr Ala				
	240	245	250	
tgc cag gct gct ggg gtc tcc gtc cac gtg tgc aat gag cac cgt tat				820
Cys Gln Ala Ala Gly Val Ser Val His Val Cys Asn Glu His Arg Tyr				
	255	260	265	
ggg tac atg aat gtg ccg gtg aaa tcc cac cag ggg ctg gaa gac gag				868
Gly Tyr Met Asn Val Pro Val Lys Ser His Gln Gly Leu Glu Asp Glu				
	270	275	280	
agg gtc aac ttc atc cac ctg atc tta gaa gca cta gtg gac ggc ccc				916
Arg Val Asn Phe Ile His Leu Ile Leu Glu Ala Leu Val Asp Gly Pro				
	285	290	295	
cgc atg cag gcc tca gct cat gtg act cgg ccc tct aag agg ccc agc				964
Arg Met Gln Ala Ser Ala His Val Thr Arg Pro Ser Lys Arg Pro Ser				
300	305	310	315	
aag ata ggg ttt gac gag gtc ttt gtc atc agc ctg gct cgc agg cct				1012
Lys Ile Gly Phe Asp Glu Val Phe Val Ile Ser Leu Ala Arg Arg Pro				
	320	325	330	
gac cgt cgg gaa cgc atg ctc gcc tcg ctc tgg gag atg gag atc tct				1060
Asp Arg Arg Glu Arg Met Leu Ala Ser Leu Trp Glu Met Glu Ile Ser				
	335	340	345	
ggg agg gtg gtg gac gct gtg gat ggc tgg atg ctc aac agc agt gcc				1108
Gly Arg Val Val Asp Ala Val Asp Gly Trp Met Leu Asn Ser Ser Ala				
	350	355	360	
atc agg aac ctc ggc gta gac ctg ctc ccg ggc tac cag gac cct tac				1156
Ile Arg Asn Leu Gly Val Asp Leu Leu Pro Gly Tyr Gln Asp Pro Tyr				
	365	370	375	
tcg ggc cgc act ctg acc aag ggc gag gtg ggc tgc ttc ctc agc cat				1204
Ser Gly Arg Thr Leu Thr Lys Gly Glu Val Gly Cys Phe Leu Ser His				
380	385	390	395	
tac tcc atc tgg gaa gag gtg gtt gcc agg ggc ctg gcc cgg gtc ctg				1252
Tyr Ser Ile Trp Glu Glu Val Val Ala Arg Gly Leu Ala Arg Val Leu				
	400	405	410	
gtg ttt gag gat gac gtg cgc ttt gag agc aac ttc agg ggg cgg ctg				1300

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Val Phe Glu Asp Asp Val Arg Phe Glu Ser Asn Phe Arg Gly Arg Leu	
415 420 425	
gag cgg ctg atg gag gat gtg gag gca gag aaa ctg tct tgg gac ctg	1348
Glu Arg Leu Met Glu Asp Val Glu Ala Glu Lys Leu Ser Trp Asp Leu	
430 435 440	
atc tac ctc gga cgg aag cag gtg aac cct gag aag gag acg gcc gtg	1396
Ile Tyr Leu Gly Arg Lys Gln Val Asn Pro Glu Lys Glu Thr Ala Val	
445 450 455	
gag ggg ctg ccg ggc ctg gtg gtg gct ggg tac tcc tac tgg acg ctg	1444
Glu Gly Leu Pro Gly Leu Val Val Ala Gly Tyr Ser Tyr Trp Thr Leu	
460 465 470 475	
gcc tat gcc ctg cgt ctg gcg ggt gcc cgc aag ctg ctg gcc tca cag	1492
Ala Tyr Ala Leu Arg Leu Ala Gly Ala Arg Lys Leu Leu Ala Ser Gln	
480 485 490	
cct ctg cgc cgc atg ctg ccc gtg gac gag ttc ctg ccc atc atg ttc	1540
Pro Leu Arg Arg Met Leu Pro Val Asp Glu Phe Leu Pro Ile Met Phe	
495 500 505	
gac cag cac ccc aac gag cag tac aag gca cac ttc tgg cca cgg gac	1588
Asp Gln His Pro Asn Glu Gln Tyr Lys Ala His Phe Trp Pro Arg Asp	
510 515 520	
ctg gtg gcc ttc tcc gcc cag ccc ctg ctc gct gcc cct acc cac tat	1636
Leu Val Ala Phe Ser Ala Gln Pro Leu Leu Ala Ala Pro Thr His Tyr	
525 530 535	
gcc ggg gac gcc gag tgg ctc agt gac acg gag aca tcc tct cca tgg	1684
Ala Gly Asp Ala Glu Trp Leu Ser Asp Thr Glu Thr Ser Ser Pro Trp	
540 545 550 555	
gat gat gac agc ggc cgc ctc atc agc tgg agc ggc tcc caa aag acc	1732
Asp Asp Asp Ser Gly Arg Leu Ile Ser Trp Ser Gly Ser Gln Lys Thr	
560 565 570	
ctg cgc agc ccc cgc ctg gac ctg act ggc agc agc ggg cac agc ctc	1780
Leu Arg Ser Pro Arg Leu Asp Leu Thr Gly Ser Ser Gly His Ser Leu	
575 580 585	
caa ccc cag ccc cga gat gag ctc taggtccagg tgaatgactgc aaagca	1830
Gln Pro Gln Pro Arg Asp Glu Leu	
590 595	

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gtgtccagga gcaggccact actgccaga gagcagagga ggaggttgtt ggcagggaact 1890
gcagatcctg tcagacctgg ccaccacott gggcatggcc actctgccct ctggacctgt 1950
ctttcatcgg gagaaaccac tcagagatgg atcccattcc ctaaaggtct cacagcaaag 2010
gagcaggact cccaggcccc tgtaccctgc ctggcctgat tcagggcctt gtggccccc 2070
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cagacatgtt gccagcaca cagtaggccc tcaataaaag ccatttgac tttaatata 2310
tatatgtatg tatatatatg tatatatata tatatatata tatgt 2355

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<210> 26

<211> 1024

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (27)...(821)

<400> 26

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                               1             5

gca ggg acc atg gcg gtg gca gca gag ctt cga gag ctg tgc cca gga 101
Ala Gly Thr Met Ala Val Ala Ala Glu Leu Arg Glu Leu Cys Pro Gly
10             15             20             25

gtg aac aac cag ccc tac ctc tgt gag agt ggt cac tgc tgc ggg gag 149
Val Asn Asn Gln Pro Tyr Leu Cys Glu Ser Gly His Cys Cys Gly Glu
30             35             40

act ggc tgc tgc acc tac tac tat gag ctc tgg tgg ttc tgg ctg ctc 197
Thr Gly Cys Cys Thr Tyr Tyr Tyr Glu Leu Trp Trp Phe Trp Leu Leu
45             50             55

tgg act gtc ctc atc ctc ttt agc tgc tgt tgc gcc ttc cgc cac cga 245
Trp Thr Val Leu Ile Leu Phe Ser Cys Cys Cys Ala Phe Arg His Arg
60             65             70

cga gct aaa ctc agg ctg caa caa cag cag cgg cag cgt gaa atc aac 293
Arg Ala Lys Leu Arg Leu Gln Gln Gln Gln Arg Gln Arg Glu Ile Asn

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75	80	85	
ttg ttg gcc tat cat ggg gca tgc cat ggg gct ggt cct ttc cct acc			341
Leu Leu Ala Tyr His Gly Ala Cys His Gly Ala Gly Pro Phe Pro Thr			
90	95	100	105
ggg tca ctg ctt gac ctt cgc ttc ctc agc acc ttc aag ccc cca gcc			389
Gly Ser Leu Leu Asp Leu Arg Phe Leu Ser Thr Phe Lys Pro Pro Ala			
110	115	120	
tac gag gat gtg gtt cac cgc cca ggc aca cca ccc ccc cct tat act			437
Tyr Glu Asp Val Val His Arg Pro Gly Thr Pro Pro Pro Pro Tyr Thr			
125	130	135	
gtg gcc cca ggc cgc ccc ttg act gct tcc agt gaa caa acc tgc tgt			485
Val Ala Pro Gly Arg Pro Leu Thr Ala Ser Ser Glu Gln Thr Cys Cys			
140	145	150	
tcc tcc tca tcc agc tgc cct gcc cac ttt gaa gga aca aat gtg gaa			533
Ser Ser Ser Ser Ser Cys Pro Ala His Phe Glu Gly Thr Asn Val Glu			
155	160	165	
ggg gtt tcc tcc cac cag agt gcc ccc ccc cat cag gag ggt gag ccc			581
Gly Val Ser Ser His Gln Ser Ala Pro Pro His Gln Glu Gly Glu Pro			
170	175	180	185
ggg gca ggg gtg acc cct gcc tcc aca ccc ccc tcc tgc cgc tat cgc			629
Gly Ala Gly Val Thr Pro Ala Ser Thr Pro Pro Ser Cys Arg Tyr Arg			
190	195	200	
cgt tta act ggc gac tcc ggt att gag ctc tgc cct tgt cct gcc tcc			677
Arg Leu Thr Gly Asp Ser Gly Ile Glu Leu Cys Pro Cys Pro Ala Ser			
205	210	215	
ggg gag ggt gag cca gtc aag gag gtg agg gtt agt gcc acc ctg cca			725
Gly Glu Gly Glu Pro Val Lys Glu Val Arg Val Ser Ala Thr Leu Pro			
220	225	230	
gat ctg gag gac tac tcc ccg tgt gca cta ccc cca gag tct gta ccg			773
Asp Leu Glu Asp Tyr Ser Pro Cys Ala Leu Pro Pro Glu Ser Val Pro			
235	240	245	
cag atc ttt ccc atg ggg ctg tct tcc agt gaa ggg gac atc cca			818
Gln Ile Phe Pro Met Gly Leu Ser Ser Ser Glu Gly Asp Ile Pro			
250	255	260	
ta agtagttttg agagggtgga tgggttactt gccaccaga aacagcccta			870

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gtcccaactc cttgcgttcc tttggccctt cctgcctac ctagaatctg cctgaaaggg 930
 ctggagaggg gcagtattgg gggactgtgc tagctttacc cccgcaggac atacacagga 990
 gcctttgatc tcattaaaga gatgtgaacc agct 1024

<210> 27

<211> 1237

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (24)...(1055)

<400> 27

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 Met Gln Pro Pro Pro Pro Gly Pro Leu Gly
 1 5 10
 gac tgc ctg cgg gac tgg gag gat cta cag cag gac ttc cag aac atc 101
 Asp Cys Leu Arg Asp Trp Glu Asp Leu Gln Gln Asp Phe Gln Asn Ile
 15 20 25
 cag gag acc cat cgg ctc tac cgc ctg aag ctg gag gag ctg acc aaa 149
 Gln Glu Thr His Arg Leu Tyr Arg Leu Lys Leu Glu Glu Leu Thr Lys
 30 35 40
 ctt cag aac aat tgc acc agc tcc atc acg cgg cag aag aag cgg ctc 197
 Leu Gln Asn Asn Cys Thr Ser Ser Ile Thr Arg Gln Lys Lys Arg Leu
 45 50 55
 cag gag ctg gcc ctc gcc ctg aag aaa tgc aaa ccc tcc ctc cca gca 245
 Gln Glu Leu Ala Leu Ala Leu Lys Lys Cys Lys Pro Ser Leu Pro Ala
 60 65 70
 gag gcc gag ggg gcc gca cag gag ctg gag aac cag atg aaa gag cgc 293
 Glu Ala Glu Gly Ala Ala Gln Glu Leu Glu Asn Gln Met Lys Glu Arg
 75 80 85 90
 caa gcc ctc ttc ttt gac atg gag gcc tat ttg cct aag aag aat gga 341
 Gln Gly Leu Phe Phe Asp Met Glu Ala Tyr Leu Pro Lys Lys Asn Gly
 95 100 105
 ttg tac ctg agc ctg gtt ctg ggg aac gtc aac gtc acg ctc ctg agc 389
 Leu Tyr Leu Ser Leu Val Leu Gly Asn Val Asn Val Thr Leu Leu Ser

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110	115	120	
aag cag gct aag ttt gcc tac aag gac gag tat gag aag ttc aag ctc			437
Lys Gln Ala Lys Phe Ala Tyr Lys Asp Glu Tyr Glu Lys Phe Lys Leu			
125	130	135	
tac ctc acc atc atc ctc atc ctc atc tcc ttc act tgc cgc ttc ctg			485
Tyr Leu Thr Ile Ile Leu Ile Leu Ile Ser Phe Thr Cys Arg Phe Leu			
140	145	150	
ctc aac tcc agg gtg aca gat gct gcc ttc aac ttc ctg ctg gtc tgg			533
Leu Asn Ser Arg Val Thr Asp Ala Ala Phe Asn Phe Leu Leu Val Trp			
155	160	165	170
tac tac tgc acc ctg acc atc cgg gag agc atc ctc atc aac aac ggc			581
Tyr Tyr Cys Thr Leu Thr Ile Arg Glu Ser Ile Leu Ile Asn Asn Gly			
175	180	185	
tcc cgg atc aaa ggc tgg tgg gtg ttc cat cac tac gtg tcc acc ttc			629
Ser Arg Ile Lys Gly Trp Trp Val Phe His His Tyr Val Ser Thr Phe			
190	195	200	
ctg tgc gga gtc atg ctg acg tgg ccc gac ggt ctc atg tac cag aaa			677
Leu Ser Gly Val Met Leu Thr Trp Pro Asp Gly Leu Met Tyr Gln Lys			
205	210	215	
ttc cgg aac caa ttc ctc tcc ttt tcc atg tac cag agc ttc gtg cag			725
Phe Arg Asn Gln Phe Leu Ser Phe Ser Met Tyr Gln Ser Phe Val Gln			
220	225	230	
ttt ctc cag tac tac tac cag agc ggc tgc ctc tac cgc ctg cgg gcg			773
Phe Leu Gln Tyr Tyr Tyr Gln Ser Gly Cys Leu Tyr Arg Leu Arg Ala			
235	240	245	250
ctg ggc gag cgg cac acc atg gac ctc act gtg gag ggc ttc cag tcc			821
Leu Gly Glu Arg His Thr Met Asp Leu Thr Val Glu Gly Phe Gln Ser			
255	260	265	
tgg atg tgg cgg ggc ctc acc ttc ctg ctg cct ttt ctt ttc ttt gga			869
Trp Met Trp Arg Gly Leu Thr Phe Leu Leu Pro Phe Leu Phe Phe Gly			
270	275	280	
cac ttc tgg cag ctt ttt aac gcg ctg acg ttg ttc aac ctg gcc cag			917
His Phe Trp Gln Leu Phe Asn Ala Leu Thr Leu Phe Asn Leu Ala Gln			
285	290	295	
gac cct cag tgc aag gag tgg cag gtg ctt atg tgc ggc ttt ccc ttc			965

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Asp Pro Gln Cys Lys Glu Trp Gln Val Leu Met Cys Gly Phe Pro Phe
 300 305 310
 ctc ctc ctt ttc ctc ggc aat ttc ttc acc acc ctg agg gtt gtg cac 1013
 Leu Leu Leu Phe Leu Gly Asn Phe Phe Thr Thr Leu Arg Val Val His
 315 320 325 330
 cac aag ttt cac agt cag cgg cac ggg agc aag aag gat tgaggctg 1060
 His Lys Phe His Ser Gln Arg His Gly Ser Lys Lys Asp
 335 340
 ggccttcccc tgccggccca gaggggcttc tgctctgtgt gttgtgggag gggatgggag 1120
 gcgccctctg agtgtgctg taccaggggg tctcttctat tctcccttg gttttatggg 1180
 cgctgtgggc cctgaaggaa gacctgggcc cagtgcctc aataaagaga ggcccag 1237

<210> 28
 <211> 1332
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (39)...(773)
 <400> 28

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 Met Asp Ile Leu Val Pro
 1 5
 ctc ctg cag ctg ctg gtg ctg ctt ctt acc ctg ccc ctg cac ctc atg 104
 Leu Leu Gln Leu Leu Val Leu Leu Leu Thr Leu Pro Leu His Leu Met
 10 15 20
 gct ctg ctg ggc tgc tgg cag ccc ctg tgc aaa agc tac ttc ccc tac 152
 Ala Leu Leu Gly Cys Trp Gln Pro Leu Cys Lys Ser Tyr Phe Pro Tyr
 25 30 35
 ctg atg gcc gtg ctg act ccc aag agc aac cgc aag atg gag agc aag 200
 Leu Met Ala Val Leu Thr Pro Lys Ser Asn Arg Lys Met Glu Ser Lys
 40 45 50
 aaa cgg gag ctc ttc agc cag ata aag ggg ctt aca gga gcc tcc ggg 248
 Lys Arg Glu Leu Phe Ser Gln Ile Lys Gly Leu Thr Gly Ala Ser Gly
 55 60 65 70

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aaa gtg gcc cta ctg gag ctg ggc tgc gga acc gga gcc aac ttt cag	296
Lys Val Ala Leu Leu Glu Leu Gly Cys Gly Thr Gly Ala Asn Phe Gln	
75 80 85	
ttc tac cca ccg ggc tgc agg gtc acc tgc cta gac cca aat ccc cac	344
Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys Leu Asp Pro Asn Pro His	
90 95 100	
ttt gag aag ttc ctg aca aag agc atg gct gag aac agg cac ctc caa	392
Phe Glu Lys Phe Leu Thr Lys Ser Met Ala Glu Asn Arg His Leu Gln	
105 110 115	
tat gag cgg ttt gtg gtg gct cct gga gag gac atg aga cag ctg gct	440
Tyr Glu Arg Phe Val Val Ala Pro Gly Glu Asp Met Arg Gln Leu Ala	
120 125 130	
gat ggc tcc atg gat gtg gtg gtc tgc act ctg gtg ctg tgc tct gtg	488
Asp Gly Ser Met Asp Val Val Val Cys Thr Leu Val Leu Cys Ser Val	
135 140 145 150	
cag agc cca agg aag gtc ctg cag gag gtc cgg aga gta ctg aga ccg	536
Gln Ser Pro Arg Lys Val Leu Gln Glu Val Arg Arg Val Leu Arg Pro	
155 160 165	
gga ggt gtg ctc ttt ttc tgg gag cat gtg gca gaa cca tat gga agc	584
Gly Gly Val Leu Phe Phe Trp Glu His Val Ala Glu Pro Tyr Gly Ser	
170 175 180	
tgg gcc ttc atg tgg cag caa gtt ttc gag ccc acc tgg aaa cac att	632
Trp Ala Phe Met Trp Gln Gln Val Phe Glu Pro Thr Trp Lys His Ile	
185 190 195	
ggg gat ggc tgc tgc ctc acc aga gag acc tgg aag gat ctt gag aac	680
Gly Asp Gly Cys Cys Leu Thr Arg Glu Thr Trp Lys Asp Leu Glu Asn	
200 205 210	
gcc cag ttc tcc gaa atc caa atg gaa cga cag ccc cct ccc ttg aag	728
Ala Gln Phe Ser Glu Ile Gln Met Glu Arg Gln Pro Pro Pro Leu Lys	
215 220 225 230	
tgg cta cct gtt ggg ccc cac atc atg gga aag gct gtc aaa taatcttcc	780
Trp Leu Pro Val Gly Pro His Ile Met Gly Lys Ala Val Lys	
235 240	
caagctccaa ggcactcatt tgctccttcc ccagcctcca attagaacaa gccacccacc	840
agcctatcta tottccactg agagggacct agcagaatga gagaagacat tcatgtacca	900

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cctactagtc cctotctccc caacctctgc cagggcaatc totaacttca atcccgcctt 960
cgacagtgaa aaagctctac ttctacgtg acccagggag gaaacactag gacctgttg 1020
tatcctcaac tgcaagtttc tggactagtc tcccaacgtt tgcctcccaa tgttgccct 1080
ttccttcgtt cccatggtaa agctcctctc gctttcctcc tgaggetaca cccatgcgtc 1140
tctaggaact ggtcacaaaa gtcatggtgc ctgcattcct gccaaagccc cctgacctc 1200
tctccccact accaccttct tcctgagctg ggggcaccag ggagaatcag agatgctggg 1260
gatgccagag caagactcaa agaggcagag gttttgttct caaatatattt ttaataaata 1320
gacgaaacca cg 1332

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<210> 29

<211> 1932

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (38)...(949)

<400> 29

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                                     1           5
aac gtg ttt ctc gcc tac ttc ctg gtg tcg atc gcc ggc ctc ctc tac 103
Asn Val Phe Leu Ala Tyr Phe Leu Val Ser Ile Ala Gly Leu Leu Tyr
          10           15           20
gag ctg gta cag ctc ggc cag cca tgt gac tgc ctt cct ccc ctg egg 151
Ala Leu Val Gln Leu Gly Gln Pro Cys Asp Cys Leu Pro Pro Leu Arg
          25           30           35
gca gca gcc gag cag cta cgg cag aag gat ctg agg att tcc cag ctg 199
Ala Ala Ala Glu Gln Leu Arg Gln Lys Asp Leu Arg Ile Ser Gln Leu
          40           45           50
caa gcg gaa ctc cga cgg cca ccc cct gcc cct gcc cag ccc cct gaa 247
Gln Ala Glu Leu Arg Arg Pro Pro Pro Ala Pro Ala Gln Pro Pro Glu
          55           60           65           70
ccc gag gcc ctg cct act atc tat gtt gtt acc ccc acc tat gcc agg 295
Pro Glu Ala Leu Pro Thr Ile Tyr Val Val Thr Pro Thr Tyr Ala Arg
          75           80           85

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ccc ctg tgg gtg cag tac cct cag gat gtg act acc ttc aat ata gat	343
Pro Leu Trp Val Gln Tyr Pro Gln Asp Val Thr Thr Phe Asn Ile Asp	
90 95 100	
gat cag tac ttg ctt ggg gat gcg ttg ctg gtt cac cct gta tca gac	391
Asp Gln Tyr Leu Leu Gly Asp Ala Leu Leu Val His Pro Val Ser Asp	
105 110 115	
tct gga gcc cat ggt gtc cag gtc tat ctg cct ggc caa ggg gag gtg	439
Ser Gly Ala His Gly Val Gln Val Tyr Leu Pro Gly Gln Gly Glu Val	
120 125 130	
tgg tat gac att caa agc tac cag aag cat cat ggt ccc cag acc ctg	487
Trp Tyr Asp Ile Gln Ser Tyr Gln Lys His His Gly Pro Gln Thr Leu	
135 140 145 150	
tac ctg cct gta act cta agc agt atc cct gtg ttc cag cgt gga ggg	535
Tyr Leu Pro Val Thr Leu Ser Ser Ile Pro Val Phe Gln Arg Gly Gly	
155 160 165	
aca atc gtg cct cga tgg atg cga gtg cgg cgg tct tca gaa tgt atg	583
Thr Ile Val Pro Arg Trp Met Arg Val Arg Arg Ser Ser Glu Cys Met	
170 175 180	
aag gat gac ccc atc act ctc ttt gtt gca ctt agc cct cag ggt aca	631
Lys Asp Asp Pro Ile Thr Leu Phe Val Ala Leu Ser Pro Gln Gly Thr	
185 190 195	
gct caa gga gag ctc ttt ctg gat gat ggg cac acg ttc aac tat cag	679
Ala Gln Gly Glu Leu Phe Leu Asp Asp Gly His Thr Phe Asn Tyr Gln	
200 205 210	
act cgc caa gag ttc ctg ctg cgt cga ttc tca ttc tct ggc aac acc	727
Thr Arg Gln Glu Phe Leu Leu Arg Arg Phe Ser Phe Ser Gly Asn Thr	
215 220 225 230	
ott gtc tcc agc tca gca gac cct gaa gga cac ttt gag aca cca atc	775
Leu Val Ser Ser Ser Ala Asp Pro Glu Gly His Phe Glu Thr Pro Ile	
235 240 245	
tgg att gag cgg gtg gtg ata ata ggg gct gga aag cca gca gct gtg	823
Trp Ile Glu Arg Val Val Ile Ile Gly Ala Gly Lys Pro Ala Ala Val	
250 255 260	
gta ctc cag aca aaa gga tct cca gaa agc cgc ctg tcc ttc cag cat	871
Val Leu Gln Thr Lys Gly Ser Pro Glu Ser Arg Leu Ser Phe Gln His	

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265	270	275	
gac cct gag acc tot gtg ttg gtc ctg cgc aag cct ggc atc aat gtg			919
Asp Pro Glu Thr Ser Val Leu Val Leu Arg Lys Pro Gly Ile Asn Val			
280	285	290	
gca tct gat tgg agt att cac ctg cga taacccaagg gatgttctgg gtta			970
Ala Ser Asp Trp Ser Ile His Leu Arg			
295	300		
gggggagggga aggggagcat tagtgctgag agatattott tcttotgcct tggagttcgg			1030
ccctccccag acttcactta tgctagtcta agaccagat tctgccaaca tttgggcagg			1090
atgagagggc tgaccotggg ctccaaattc ctcttgatgat ctctcactct cctccactcc			1150
attgatacca actctttccc ttcattcccc caacatcctg ttgctctaac tggagcacat			1210
tcacttacga acaccaggaa accacagggc ccttgctgcc ccttctcttt cccttattta			1270
ggagccctga actccccag agtctatcca ttcattgcctc ttgtatgttg atgccacttc			1330
ttggaagaag atgagggcaa tgagttaggg ctctctttcc ccttccctcc caccagattg			1390
ctctccacc tttcattttct tctccaggc tttactcccc tttttatgcc ccaccgatac			1450
actgggacca ccccttacct cggacaggat gaatggatca aaggagtga gttgctaaag			1510
aacatccttt tccctctcat totacccttt tctctctccc gattccttgt agagctgctg			1570
caattcttag aggggcagtt ctacctctc tgtccctcgg cagaaagacg tttccacacc			1630
tcttagggga tgcgcattaa acttcttttg cccctctctt gtccctttg aggggcactt			1690
aagatggaga aatcagttgt ggtttcagtg aatcatggtc acctgtattt attgctagga			1750
gaagcctgag ggtgggggga gatgatcatg tgtgctcggg gttggctgga agccctgggt			1810
ggggggttg gggaggacta atggggagtc ggggaatatt tgtgggtatt ttttttactt			1870
cctcttggtt cccagctgtg acacgttttg atcaaaggag aaacaataaa gggataaacc			1930
at			1932

<210> 30

<211> 1124

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (73)...(555)

<400> 30

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gactgggccc ca atg gac aag ctg aag aag gtg ctg agc ggg cag gac acg	111

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Met Asp Lys Leu Lys Lys Val Leu Ser Gly Gln Asp Thr									
1		5		10					
gag gac cgg agc ggc ctg tcc gag gtt gtt gag gca tct tca tta agc						159			
Glu Asp Arg Ser Gly Leu Ser Glu Val Val Glu Ala Ser Ser Leu Ser									
15		20		25					
tgg agt acc agg ata aaa ggc ttc att gcg tgt ttt gct ata gga att						207			
Trp Ser Thr Arg Ile Lys Gly Phe Ile Ala Cys Phe Ala Ile Gly Ile									
30		35		40		45			
ctc tgc tca ctg ctg ggt act gtt ctg ctg tgg gtg ccc agg aag gga						255			
Leu Cys Ser Leu Leu Gly Thr Val Leu Leu Trp Val Pro Arg Lys Gly									
50		55		60					
cta cac ctc ttc gca gtg ttt tat acc ttt ggt aat atc gca tca att						303			
Leu His Leu Phe Ala Val Phe Tyr Thr Phe Gly Asn Ile Ala Ser Ile									
65		70		75					
ggg agt acc atc ttc ctc atg gga cca gtg aaa cag ctg aag cga atg						351			
Gly Ser Thr Ile Phe Leu Met Gly Pro Val Lys Gln Leu Lys Arg Met									
80		85		90					
ttt gag cot act cgt ttg att gca act atc atg gtg ctg ttg tgt ttt						399			
Phe Glu Pro Thr Arg Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe									
95		100		105					
gca ctt acc ctg tgt tct gcc ttt tgg tgg cat aac aag gga ctt gca						447			
Ala Leu Thr Leu Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala									
110		115		120		125			
ctt atc ttc tgc att ttg cag tct ttg gca ttg acg tgg tac agc ctt						495			
Leu Ile Phe Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu									
130		135		140					
tcc ttc ata cca ttt gca agg gat gct gtg aag aag tgt ttt gcc gtg						543			
Ser Phe Ile Pro Phe Ala Arg Asp Ala Val Lys Lys Cys Phe Ala Val									
145		150		155					
tgt ctt gca taattcatgg ccagttttat gaagctttgg aaggcactat ggacagaa						600			
Cys Leu Ala									
160									
gctggtggac agttttgtaa ctatcttcga aacctctgtc ttacagacat gtgcctttta						660			
tcttgacgca atgtgttget tgtgattcga acatttgagg gttacttttg gaagcaacaa						720			
tacattctcg aacctgaatg tcagtagcac aggatgagaa gtgggttctg tatcttgtgg						780			

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agtggaatct tcctcatgta cctgtttcct ctctggatgt tgtcccactg aattcccatg      840
aatacaaacc tattcagcaa cagcacataa gccttgggtg caagtgattc ccaggtggca      900
aaaggcagcc ccatcagaga tcacgggagc aacagtaagg gacagagttt tgggggtccac      960
ttgtccctca gcatggaagc catcacctg gtctgcata gagtgagtct acttctactc     1020
tggcatctga gaacaagtga ctctgcttta gacaagcccc tggagagcct ggccatggag     1080
tgaggtagaa aagaagcact ttttggtggt atatgctgtt tctg                      1124

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<210> 31

<211> 1445

<212> PRT

<213> Homo sapiens

<400> 31

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Met Gln Gly Pro Pro Leu Leu Thr Ala Ala His Leu Leu Cys Val Cys
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Thr Ala Ala Leu Ala Val Ala Pro Gly Pro Arg Phe Leu Val Thr Ala
              20              25              30
Pro Gly Ile Ile Arg Pro Gly Gly Asn Val Thr Ile Gly Val Glu Leu
              35              40              45
Leu Glu His Cys Pro Ser Gln Val Thr Val Lys Ala Glu Leu Leu Lys
              50              55              60
Thr Ala Ser Asn Leu Thr Val Ser Val Leu Glu Ala Glu Gly Val Phe
              65              70              75              80
Glu Lys Gly Ser Phe Lys Thr Leu Thr Leu Pro Ser Leu Pro Leu Asn
              85              90              95
Ser Ala Asp Glu Ile Tyr Glu Leu Arg Val Thr Gly Arg Thr Gln Asp
              100              105              110
Glu Ile Leu Phe Ser Asn Ser Thr Arg Leu Ser Phe Glu Thr Lys Arg
              115              120              125
Ile Ser Val Phe Ile Gln Thr Asp Lys Ala Leu Tyr Lys Pro Lys Gln
              130              135              140
Glu Val Lys Phe Arg Ile Val Thr Leu Phe Ser Asp Phe Lys Pro Tyr
              145              150              155              160
Lys Thr Ser Leu Asn Ile Leu Ile Lys Asp Pro Lys Ser Asn Leu Ile
              165              170              175
Gln Gln Trp Leu Ser Gln Gln Ser Asp Leu Gly Val Ile Ser Lys Thr

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180	185	190
Phe Gln Leu Ser Ser His Pro Ile Leu Gly Asp Trp Ser Ile Gln Val		
195	200	205
Gln Val Asn Asp Gln Thr Tyr Tyr Gln Ser Phe Gln Val Ser Glu Tyr		
210	215	220
Val Leu Pro Lys Phe Glu Val Thr Leu Gln Thr Pro Leu Tyr Cys Ser		
225	230	235
Met Asn Ser Lys His Leu Asn Gly Thr Ile Thr Ala Lys Tyr Thr Tyr		
245	250	255
Gly Lys Pro Val Lys Gly Asp Val Thr Leu Thr Phe Leu Pro Leu Ser		
260	265	270
Phe Trp Gly Lys Lys Lys Asn Ile Thr Lys Thr Phe Lys Ile Asn Gly		
275	280	285
Ser Ala Asn Phe Ser Phe Asn Asp Glu Glu Met Lys Asn Val Met Asp		
290	295	300
Ser Ser Asn Gly Leu Ser Glu Tyr Leu Asp Leu Ser Phe Pro Gly Pro		
305	310	315
Val Glu Ile Leu Thr Thr Val Thr Glu Ser Val Thr Gly Ile Ser Arg		
325	330	335
Asn Val Ser Thr Asn Val Phe Phe Lys Gln His Asp Tyr Ile Ile Glu		
340	345	350
Phe Phe Asp Tyr Thr Thr Val Leu Lys Pro Ser Leu Asn Phe Thr Ala		
355	360	365
Thr Val Lys Val Thr Arg Ala Asp Gly Asn Gln Leu Thr Leu Glu Glu		
370	375	380
Arg Arg Asn Asn Val Val Ile Thr Val Thr Gln Arg Asn Tyr Thr Glu		
385	390	395
Tyr Trp Ser Gly Ser Asn Ser Gly Asn Gln Lys Met Glu Ala Val Gln		
405	410	415
Lys Ile Asn Tyr Thr Val Pro Gln Ser Gly Thr Phe Lys Ile Glu Phe		
420	425	430
Pro Ile Leu Glu Asp Ser Ser Glu Leu Gln Leu Lys Ala Tyr Phe Leu		
435	440	445
Gly Ser Lys Ser Ser Met Ala Val His Ser Leu Phe Lys Ser Pro Ser		
450	455	460

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Lys Thr Tyr Ile Gln Leu Lys Thr Arg Asp Glu Asn Ile Lys Val Gly
 465 470 475 480
 Ser Pro Phe Glu Leu Val Val Ser Gly Asn Lys Arg Leu Lys Glu Leu
 485 490 495
 Ser Tyr Met Val Val Ser Arg Gly Gln Leu Val Ala Val Gly Lys Gln
 500 505 510
 Asn Ser Thr Met Phe Ser Leu Thr Pro Glu Asn Ser Trp Thr Pro Lys
 515 520 525
 Ala Cys Val Ile Val Tyr Tyr Ile Glu Asp Asp Gly Glu Ile Ile Ser
 530 535 540
 Asp Val Leu Lys Ile Pro Val Gln Leu Val Phe Lys Asn Lys Ile Lys
 545 550 555 560
 Leu Tyr Trp Ser Lys Val Lys Ala Glu Pro Ser Glu Lys Val Ser Leu
 565 570 575
 Arg Ile Ser Val Thr Gln Pro Asp Ser Ile Val Gly Ile Val Ala Val
 580 585 590
 Asp Lys Ser Val Asn Leu Met Asn Ala Ser Asn Asp Ile Thr Met Glu
 595 600 605
 Asn Val Val His Glu Leu Glu Leu Tyr Asn Thr Gly Tyr Tyr Leu Gly
 610 615 620
 Met Phe Met Asn Ser Phe Ala Val Phe Gln Glu Cys Gly Leu Trp Val
 625 630 635 640
 Leu Thr Asp Ala Asn Leu Thr Lys Asp Tyr Ile Asp Gly Val Tyr Asp
 645 650 655
 Asn Ala Glu Tyr Ala Glu Arg Phe Met Glu Glu Asn Glu Gly His Ile
 660 665 670
 Val Asp Ile His Asp Phe Ser Leu Gly Ser Ser Pro His Val Arg Lys
 675 680 685
 His Phe Pro Glu Thr Trp Ile Trp Leu Asp Thr Asn Met Gly Ser Arg
 690 695 700
 Ile Tyr Gln Glu Phe Glu Val Thr Val Pro Asp Ser Ile Thr Ser Trp
 705 710 715 720
 Val Ala Thr Gly Phe Val Ile Ser Glu Asp Leu Gly Leu Gly Leu Thr
 725 730 735
 Thr Thr Pro Val Glu Leu Gln Ala Phe Gln Pro Phe Phe Ile Phe Leu

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740	745	750
Asn Leu Pro Tyr Ser Val Ile Arg Gly Glu Glu Phe Ala Leu Glu Ile		
755	760	765
Thr Ile Phe Asn Tyr Leu Lys Asp Ala Thr Glu Val Lys Val Ile Ile		
770	775	780
Glu Lys Ser Asp Lys Phe Asp Ile Leu Met Thr Ser Ser Glu Ile Asn		
785	790	795
Ala Thr Gly His Gln Gln Thr Leu Leu Val Pro Ser Glu Asp Gly Ala		
805	810	815
Thr Val Leu Phe Pro Ile Arg Pro Thr His Leu Gly Glu Ile Pro Ile		
820	825	830
Thr Val Thr Ala Leu Ser Pro Thr Ala Ser Asp Ala Ile Thr Gln Met		
835	840	845
Ile Leu Val Lys Ala Glu Gly Ile Glu Lys Ser Tyr Ser Gln Ser Ile		
850	855	860
Leu Leu Asp Leu Thr Asp Asn Arg Leu Gln Ser Thr Leu Lys Thr Leu		
865	870	875
Ser Phe Ser Phe Pro Pro Asn Thr Val Thr Gly Ser Glu Arg Val Gln		
885	890	895
Ile Thr Ala Ile Gly Asp Val Leu Gly Pro Ser Ile Asn Gly Leu Ala		
900	905	910
Ser Leu Ile Arg Met Pro Tyr Gly Cys Gly Glu Gln Asn Met Ile Asn		
915	920	925
Phe Ala Pro Asn Ile Tyr Ile Leu Asp Tyr Leu Thr Lys Lys Lys Gln		
930	935	940
Leu Thr Asp Asn Leu Lys Glu Lys Ala Leu Ser Phe Met Arg Gln Gly		
945	950	955
Tyr Gln Arg Glu Leu Leu Tyr Gln Arg Glu Asp Gly Ser Phe Ser Ala		
965	970	975
Phe Gly Asn Tyr Asp Pro Ser Gly Ser Thr Trp Leu Ser Ala Phe Val		
980	985	990
Leu Arg Cys Phe Leu Glu Ala Asp Pro Tyr Ile Asp Ile Asp Gln Asn		
995	1000	1005
Val Leu His Arg Thr Tyr Thr Trp Leu Lys Gly His Gln Lys Ser Asn		
1010	1015	1020

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Gly Glu Phe Trp Asp Pro Gly Arg Val Ile His Ser Glu Leu Gln Gly
 1025 1030 1035 1040
 Gly Asn Lys Ser Pro Val Thr Leu Thr Ala Tyr Ile Val Thr Ser Leu
 1045 1050 1055
 Leu Gly Tyr Arg Lys Tyr Gln Pro Asn Ile Asp Val Gln Glu Ser Ile
 1060 1065 1070
 His Phe Leu Glu Ser Glu Phe Ser Arg Gly Ile Ser Asp Asn Tyr Thr
 1075 1080 1085
 Leu Ala Leu Ile Thr Tyr Ala Leu Ser Ser Val Gly Ser Pro Lys Ala
 1090 1095 1100
 Lys Glu Ala Leu Asn Met Leu Thr Trp Arg Ala Glu Gln Glu Gly Gly
 1105 1110 1115 1120
 Met Gln Phe Trp Val Ser Ser Glu Ser Lys Leu Ser Asp Ser Trp Gln
 1125 1130 1135
 Pro Arg Ser Leu Asp Ile Glu Val Ala Ala Tyr Ala Leu Leu Ser His
 1140 1145 1150
 Phe Leu Gln Phe Gln Thr Ser Glu Gly Ile Pro Ile Met Arg Trp Leu
 1155 1160 1165
 Ser Arg Gln Arg Asn Ser Leu Gly Gly Phe Ala Ser Thr Gln Asp Thr
 1170 1175 1180
 Thr Val Ala Leu Lys Ala Leu Ser Glu Phe Ala Ala Leu Met Asn Thr
 1185 1190 1195 1200
 Glu Arg Thr Asn Ile Gln Val Thr Val Thr Gly Pro Ser Ser Pro Ser
 1205 1210 1215
 Pro Val Lys Phe Leu Ile Asp Thr His Asn Arg Leu Leu Leu Gln Thr
 1220 1225 1230
 Ala Glu Leu Ala Val Val Gln Pro Thr Ala Val Asn Ile Ser Ala Asn
 1235 1240 1245
 Gly Phe Gly Phe Ala Ile Cys Gln Leu Asn Val Val Tyr Asn Val Lys
 1250 1255 1260
 Ala Ser Gly Ser Ser Arg Arg Arg Arg Ser Ile Gln Asn Gln Glu Ala
 1265 1270 1275 1280
 Phe Asp Leu Asp Val Ala Val Lys Glu Asn Lys Asp Asp Leu Asn His
 1285 1290 1295
 Val Asp Leu Asn Val Cys Thr Ser Phe Ser Gly Pro Gly Arg Ser Gly

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1300 1305 1310
 Met Ala Leu Met Glu Val Asn Leu Leu Ser Gly Phe Met Val Pro Ser
 1315 1320 1325
 Glu Ala Ile Ser Leu Ser Glu Thr Val Lys Lys Val Glu Tyr Asp His
 1330 1335 1340
 Gly Lys Leu Asn Leu Tyr Leu Asp Ser Val Asn Glu Thr Gln Phe Cys
 1345 1350 1355 1360
 Val Asn Ile Pro Ala Val Arg Asn Phe Lys Val Ser Asn Thr Gln Asp
 1365 1370 1375
 Ala Ser Val Ser Ile Val Asp Tyr Tyr Glu Pro Arg Arg Gln Ala Val
 1380 1385 1390
 Arg Ser Tyr Asn Ser Glu Val Lys Leu Ser Ser Cys Asp Leu Cys Ser
 1395 1400 1405
 Asp Val Gln Gly Cys Arg Pro Cys Glu Asp Gly Ala Ser Gly Ser His
 1410 1415 1420
 His His Ser Ser Val Ile Phe Ile Phe Cys Phe Lys Leu Leu Tyr Phe
 1425 1430 1435 1440
 Met Glu Leu Trp Leu
 1445

<210> 32

<211> 582

<212> PRT

<213> Homo sapiens

<400> 32

Met Phe Pro Ala Gly Pro Pro Ser His Ser Leu Leu Arg Leu Pro Leu
 1 5 10 15
 Leu Gln Leu Leu Leu Leu Val Val Gln Ala Val Gly Arg Gly Leu Gly
 20 25 30
 Arg Ala Ser Pro Ala Gly Gly Pro Leu Glu Asp Val Val Ile Glu Arg
 35 40 45
 Tyr His Ile Pro Arg Ala Cys Pro Arg Glu Val Gln Met Gly Asp Phe
 50 55 60
 Val Arg Tyr His Tyr Asn Gly Thr Phe Glu Asp Gly Lys Lys Phe Asp
 65 70 75 80

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Ser Ser Tyr Asp Arg Asn Thr Leu Val Ala Ile Val Val Gly Val Gly
 85 90 95
 Arg Leu Ile Thr Gly Met Asp Arg Gly Leu Met Gly Met Cys Val Asn
 100 105 110
 Glu Arg Arg Arg Leu Ile Val Pro Pro His Leu Gly Tyr Gly Ser Ile
 115 120 125
 Gly Leu Ala Gly Leu Ile Pro Pro Asp Ala Thr Leu Tyr Phe Asp Val
 130 135 140
 Val Leu Leu Asp Val Trp Asn Lys Glu Asp Thr Val Gln Val Ser Thr
 145 150 155 160
 Leu Leu Arg Pro Pro His Cys Pro Arg Met Val Gln Asp Gly Asp Phe
 165 170 175
 Val Arg Tyr His Tyr Asn Gly Thr Leu Leu Asp Gly Thr Ser Phe Asp
 180 185 190
 Thr Ser Tyr Ser Lys Gly Gly Thr Tyr Asp Thr Tyr Val Gly Ser Gly
 195 200 205
 Trp Leu Ile Lys Gly Met Asp Gln Gly Leu Leu Gly Met Cys Pro Gly
 210 215 220
 Glu Arg Arg Lys Ile Ile Ile Pro Pro Phe Leu Ala Tyr Gly Glu Lys
 225 230 235 240
 Gly Tyr Gly Thr Val Ile Pro Pro Gln Ala Ser Leu Val Phe His Val
 245 250 255
 Leu Leu Ile Asp Val His Asn Pro Lys Asp Ala Val Gln Leu Glu Thr
 260 265 270
 Leu Glu Leu Pro Pro Gly Cys Val Arg Arg Ala Gly Ala Gly Asp Phe
 275 280 285
 Met Arg Tyr His Tyr Asn Gly Ser Leu Met Asp Gly Thr Leu Phe Asp
 290 295 300
 Ser Ser Tyr Ser Arg Asn His Thr Tyr Asn Thr Tyr Ile Gly Gln Gly
 305 310 315 320
 Tyr Ile Ile Pro Gly Met Asp Gln Gly Leu Gln Gly Ala Cys Met Gly
 325 330 335
 Glu Arg Arg Arg Ile Thr Ile Pro Pro His Leu Ala Tyr Gly Glu Asn
 340 345 350
 Gly Thr Gly Asp Lys Ile Pro Gly Ser Ala Val Leu Ile Phe Asn Val

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355	360	365
His Val Ile Asp Phe	His Asn Pro Ala Asp Val Val	Glu Ile Arg Thr
370	375	380
Leu Ser Arg Pro Ser	Glu Thr Cys Asn Glu Thr Thr	Lys Leu Gly Asp
385	390	395
Phe Val Arg Tyr His	Tyr Asn Cys Ser Leu Leu Asp Gly Thr	Gln Leu
405	410	415
Phe Thr Ser His Asp	Tyr Gly Ala Pro Gln Glu Ala Thr	Leu Gly Ala
420	425	430
Asn Lys Val Ile Glu	Gly Leu Asp Thr Gly Leu Gln Gly Met	Cys Val
435	440	445
Gly Glu Arg Arg Gln	Leu Ile Val Pro Pro His Leu Ala His	Gly Glu
450	455	460
Ser Gly Ala Arg Gly	Val Pro Gly Ser Ala Val Leu Leu Phe	Glu Val
465	470	475
Glu Leu Val Ser Arg	Glu Asp Gly Leu Pro Thr Gly Tyr Leu	Phe Val
485	490	495
Trp His Lys Asp Pro	Pro Ala Asn Leu Phe Glu Asp Met Asp	Leu Asn
500	505	510
Lys Asp Gly Glu Val	Pro Pro Glu Glu Phe Ser Thr Phe Ile	Lys Ala
515	520	525
Gln Val Ser Glu Gly	Lys Gly Arg Leu Met Pro Gly Gln Asp	Pro Glu
530	535	540
Lys Thr Ile Gly Asp	Met Phe Gln Asn Gln Asp Arg Asn Gln	Asp Gly
545	550	555
Lys Ile Thr Val Asp	Glu Leu Lys Leu Lys Ser Asp Glu Asp	Glu Glu
565	570	575
Arg Val His Glu Glu	Leu	
580		

<210> 33

<211> 410

<212> PRT

<213> Homo sapiens

<400> 33

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Met Glu Leu Pro Ser Gly Pro Gly Pro Glu Arg Leu Phe Asp Ser His
 1 5 10 15
 Arg Leu Pro Gly Asp Cys Phe Leu Leu Leu Val Leu Leu Leu Tyr Ala
 20 25 30
 Pro Val Gly Phe Cys Leu Leu Val Leu Arg Leu Phe Leu Gly Ile His
 35 40 45
 Val Phe Leu Val Ser Cys Ala Leu Pro Asp Ser Val Leu Arg Arg Phe
 50 55 60
 Val Val Arg Thr Met Cys Ala Val Leu Gly Leu Val Ala Arg Gln Glu
 65 70 75 80
 Asp Ser Gly Leu Arg Asp His Ser Val Arg Val Leu Ile Ser Asn His
 85 90 95
 Val Thr Pro Phe Asp His Asn Ile Val Asn Leu Leu Thr Thr Cys Ser
 100 105 110
 Thr Pro Leu Leu Asn Ser Pro Pro Ser Phe Val Cys Trp Ser Arg Gly
 115 120 125
 Phe Met Glu Met Asn Gly Arg Gly Glu Leu Val Glu Ser Leu Lys Arg
 130 135 140
 Phe Cys Ala Ser Thr Arg Leu Pro Pro Thr Pro Leu Leu Leu Phe Pro
 145 150 155 160
 Glu Glu Glu Ala Thr Asn Gly Arg Glu Gly Leu Leu Arg Phe Ser Ser
 165 170 175
 Trp Pro Phe Ser Ile Gln Asp Val Val Gln Pro Leu Thr Leu Gln Val
 180 185 190
 Gln Arg Pro Leu Val Ser Val Thr Val Ser Asp Ala Ser Trp Val Ser
 195 200 205
 Glu Leu Leu Trp Ser Leu Phe Val Pro Phe Thr Val Tyr Gln Val Arg
 210 215 220
 Trp Leu Arg Pro Val His Arg Gln Leu Gly Glu Ala Asn Glu Glu Phe
 225 230 235 240
 Ala Leu Arg Val Gln Gln Leu Val Ala Lys Glu Leu Gly Gln Thr Gly
 245 250 255
 Thr Arg Leu Thr Pro Ala Asp Lys Ala Glu His Met Lys Arg Gln Arg
 260 265 270
 His Pro Arg Leu Arg Pro Gln Ser Ala Gln Ser Ser Phe Pro Pro Ser

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275	280	285
Pro Gly Pro Ser Pro Asp Val Gln Leu Ala Thr Leu Ala Gln Arg Val		
290	295	300
Lys Glu Val Leu Pro His Val Pro Leu Gly Val Ile Gln Arg Asp Leu		
305	310	315
Ala Lys Thr Gly Cys Val Asp Leu Thr Ile Thr Asn Leu Leu Glu Gly		
325	330	335
Ala Val Ala Phe Met Pro Glu Asp Ile Thr Lys Gly Thr Gln Ser Leu		
340	345	350
Pro Thr Ala Ser Ala Ser Lys Phe Pro Ser Ser Gly Pro Val Thr Pro		
355	360	365
Gln Pro Thr Ala Leu Thr Phe Ala Lys Ser Ser Trp Ala Arg Gln Glu		
370	375	380
Ser Leu Gln Glu Arg Lys Gln Ala Leu Tyr Glu Tyr Ala Arg Arg Arg		
385	390	395
Phe Thr Glu Arg Arg Ala Gln Glu Ala Asp		
405	410	

<210> 34

<211> 483

<212> PRT

<213> Homo sapiens

<400> 34

Met Glu Glu Gly Gly Gly Gly Val Arg Ser Leu Val Pro Gly Gly Pro		
1	5	10
Val Leu Leu Val Leu Cys Gly Leu Leu Glu Ala Ser Gly Gly Gly Arg		
20	25	30
Ala Leu Pro Gln Leu Ser Asp Asp Ile Pro Phe Arg Val Asn Trp Pro		
35	40	45
Gly Thr Glu Phe Ser Leu Pro Thr Thr Gly Val Leu Tyr Lys Glu Asp		
50	55	60
Asn Tyr Val Ile Met Thr Thr Ala His Lys Glu Lys Tyr Lys Cys Ile		
65	70	75
Leu Pro Leu Val Thr Ser Gly Asp Glu Glu Glu Glu Lys Asp Tyr Lys		
85	90	95

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Gly Pro Asn Pro Arg Glu Leu Leu Glu Pro Leu Phe Lys Gln Ser Ser
 100 105 110
 Cys Ser Tyr Arg Ile Glu Ser Tyr Trp Thr Tyr Glu Val Cys His Gly
 115 120 125
 Lys His Ile Arg Gln Tyr His Glu Glu Lys Glu Thr Gly Gln Lys Ile
 130 135 140
 Asn Ile His Glu Tyr Tyr Leu Gly Asn Met Leu Ala Lys Asn Leu Leu
 145 150 155 160
 Phe Glu Lys Glu Arg Glu Ala Glu Glu Lys Glu Lys Ser Asn Glu Ile
 165 170 175
 Pro Thr Lys Asn Ile Glu Gly Gln Met Thr Pro Tyr Tyr Pro Val Gly
 180 185 190
 Met Gly Asn Gly Thr Pro Cys Ser Leu Lys Gln Asn Arg Pro Arg Ser
 195 200 205
 Ser Thr Val Met Tyr Ile Cys His Pro Glu Ser Lys His Glu Ile Leu
 210 215 220
 Ser Val Ala Glu Val Thr Thr Cys Glu Tyr Glu Val Val Ile Leu Thr
 225 230 235 240
 Pro Leu Leu Cys Ser His Pro Lys Tyr Arg Phe Arg Ala Ser Pro Val
 245 250 255
 Asn Asp Ile Phe Cys Gln Ser Leu Pro Gly Ser Pro Phe Lys Pro Leu
 260 265 270
 Thr Leu Arg Gln Leu Glu Gln Gln Glu Glu Ile Leu Arg Val Pro Phe
 275 280 285
 Arg Arg Asn Lys Glu Glu Asp Leu Gln Ser Thr Lys Glu Glu Arg Phe
 290 295 300
 Pro Ala Ile His Lys Ser Ile Ala Ile Gly Ser Gln Pro Val Leu Thr
 305 310 315 320
 Val Gly Thr Thr His Ile Ser Lys Leu Thr Asp Asp Gln Leu Ile Lys
 325 330 335
 Glu Phe Leu Ser Gly Ser Tyr Cys Phe Arg Gly Gly Val Gly Trp Trp
 340 345 350
 Lys Tyr Glu Phe Cys Tyr Gly Lys His Val His Gln Tyr His Glu Asp
 355 360 365
 Lys Asp Ser Gly Lys Thr Ser Val Val Val Gly Thr Trp Asn Gln Glu

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370 375 380
 Glu His Ile Glu Trp Ala Lys Lys Asn Thr Ala Arg Ala Tyr His Leu
 385 390 395 400
 Gln Asp Asp Gly Thr Gln Thr Val Arg Met Val Ser His Phe Tyr Gly
 405 410 415
 Asn Gly Asp Ile Cys Asp Ile Thr Asp Lys Pro Arg Gln Val Thr Val
 420 425 430
 Lys Leu Lys Cys Lys Glu Ser Asp Ser Pro His Ala Val Thr Val Tyr
 435 440 445
 Met Leu Glu Pro His Ser Cys Gln Tyr Ile Leu Gly Val Glu Ser Pro
 450 455 460
 Val Ile Cys Lys Ile Leu Asp Thr Ala Asp Glu Asn Gly Leu Leu Ser
 465 470 475 480
 Leu Pro Asn

<210> 35

<211> 607

<212> PRT

<213> Homo sapiens

<400> 35

Met Gly Phe Glu Glu Leu Leu Glu Gln Val Gly Gly Phe Gly Pro Phe
 1 5 10 15
 Gln Leu Arg Asn Val Ala Leu Leu Ala Leu Pro Arg Val Leu Leu Pro
 20 25 30
 Leu His Phe Leu Leu Pro Ile Phe Leu Ala Ala Val Pro Ala His Arg
 35 40 45
 Cys Ala Leu Pro Gly Ala Pro Ala Asn Phe Ser His Gln Asp Val Trp
 50 55 60
 Leu Glu Ala His Leu Pro Arg Glu Pro Asp Gly Thr Leu Ser Ser Cys
 65 70 75 80
 Leu Arg Phe Ala Tyr Pro Gln Ala Leu Pro Asn Thr Thr Leu Gly Glu
 85 90 95
 Glu Arg Gln Ser Arg Gly Glu Leu Glu Asp Glu Pro Ala Thr Val Pro
 100 105 110

60/233

Cys Ser Gln Gly Trp Glu Tyr Asp His Ser Glu Phe Ser Ser Thr Ile
 115 120 125
 Ala Thr Glu Ser Gln Val Gly Ile Tyr Ile Ile His Leu Glu Val Glu
 130 135 140
 Cys Arg Trp Arg Gln Ser Pro Trp Glu Ala Ala Gly Arg Gly Leu Pro
 145 150 155 160
 Trp Glu Glu Ala Glu Ala Ala Gly Leu Gly Arg Asp Lys Val Ser Tyr
 165 170 175
 Ser Pro Ser Trp Arg Glu Ser Leu Gly Gly Leu Leu Ser Gly Met Glu
 180 185 190
 Trp Asp Leu Val Cys Glu Gln Lys Gly Leu Asn Arg Ala Ala Ser Thr
 195 200 205
 Phe Phe Phe Ala Gly Val Leu Val Gly Ala Val Ala Phe Gly Tyr Leu
 210 215 220
 Ser Asp Arg Phe Gly Arg Arg Arg Leu Leu Leu Val Ala Tyr Val Ser
 225 230 235 240
 Thr Leu Val Leu Gly Leu Ala Ser Ala Ala Ser Val Ser Tyr Val Met
 245 250 255
 Phe Ala Ile Thr Arg Thr Leu Thr Gly Ser Ala Leu Ala Gly Phe Thr
 260 265 270
 Ile Ile Val Met Pro Leu Glu Leu Glu Trp Leu Asp Val Glu His Arg
 275 280 285
 Thr Val Ala Gly Val Leu Ser Ser Thr Phe Trp Thr Gly Gly Val Met
 290 295 300
 Leu Leu Ala Leu Val Gly Tyr Leu Ile Arg Asp Trp Arg Trp Leu Leu
 305 310 315 320
 Leu Ala Val Thr Leu Pro Cys Ala Pro Gly Ile Leu Ser Leu Trp Trp
 325 330 335
 Val Pro Glu Ser Ala Arg Trp Leu Leu Thr Gln Gly His Val Lys Glu
 340 345 350
 Ala His Arg Tyr Leu Leu His Cys Ala Arg Leu Asn Gly Arg Pro Val
 355 360 365
 Cys Glu Asp Ser Phe Ser Gln Glu Ala Val Ser Lys Val Ala Ala Gly
 370 375 380
 Glu Arg Val Val Arg Arg Pro Ser Tyr Leu Asp Leu Phe Arg Thr Pro

61/233

385 390 395 400
 Arg Leu Arg His Ile Ser Leu Cys Cys Val Val Val Trp Phe Gly Val
 405 410 415
 Asn Phe Ser Tyr Tyr Gly Leu Ser Leu Asp Val Ser Gly Leu Gly Leu
 420 425 430
 Asn Val Tyr Gln Thr Gln Leu Leu Phe Gly Ala Val Glu Leu Pro Ser
 435 440 445
 Lys Leu Leu Val Tyr Leu Ser Val Arg Tyr Ala Gly Arg Arg Leu Thr
 450 455 460
 Gln Ala Gly Thr Leu Leu Gly Thr Ala Leu Ala Phe Gly Thr Arg Leu
 465 470 475 480
 Leu Val Ser Ser Asp Met Lys Ser Trp Ser Thr Val Leu Ala Val Met
 485 490 495
 Gly Lys Ala Phe Ser Glu Ala Ala Phe Thr Thr Ala Tyr Leu Phe Thr
 500 505 510
 Ser Glu Leu Tyr Pro Thr Val Leu Arg Gln Thr Gly Met Gly Leu Thr
 515 520 525
 Ala Leu Val Gly Arg Leu Gly Gly Ser Leu Ala Pro Leu Ala Ala Leu
 530 535 540
 Leu Asp Gly Val Trp Leu Ser Leu Pro Lys Leu Thr Tyr Gly Gly Ile
 545 550 555 560
 Ala Leu Leu Ala Ala Gly Thr Ala Leu Leu Leu Pro Glu Thr Arg Gln
 565 570 575
 Ala Gln Leu Pro Glu Thr Ile Gln Asp Val Glu Arg Lys Ser Ala Pro
 580 585 590
 Thr Ser Leu Gln Glu Glu Glu Met Pro Met Lys Gln Val Gln Asn
 595 600 605

<210> 36

<211> 314

<212> PRT

<213> Homo sapiens

<400> 36

Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Ala Arg Ala

1

5

10

15

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Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser Gly Pro
 20 25 30
 Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly Glu Asp Ala
 35 40 45
 Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg Leu Trp Asp Ser
 50 55 60
 His Val Cys Gly Val Ser Leu Leu Ser His Arg Trp Ala Leu Thr Ala
 65 70 75 80
 Ala His Cys Phe Glu Thr Tyr Ser Asp Leu Ser Asp Pro Ser Gly Trp
 85 90 95
 Met Val Gln Phe Gly Gln Leu Thr Ser Met Pro Ser Phe Trp Ser Leu
 100 105 110
 Gln Ala Tyr Tyr Thr Arg Tyr Phe Val Ser Asn Ile Tyr Leu Ser Pro
 115 120 125
 Arg Tyr Leu Gly Asn Ser Pro Tyr Asp Ile Ala Leu Val Lys Leu Ser
 130 135 140
 Ala Pro Val Thr Tyr Thr Lys His Ile Gln Pro Ile Cys Leu Gln Ala
 145 150 155 160
 Ser Thr Phe Glu Phe Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp
 165 170 175
 Gly Tyr Ile Lys Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln
 180 185 190
 Glu Val Gln Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe
 195 200 205
 Leu Lys Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala
 210 215 220
 Gly Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
 225 230 235 240
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val Val
 245 250 255
 Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val Tyr Thr
 260 265 270
 Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met Ala Gln Ser
 275 280 285
 Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu Phe Phe Pro Leu

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290 295 300
 Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
 305 310

 <210> 37
 <211> 94
 <212> PRT
 <213> Homo sapiens
 <400> 37
 Met Glu Leu Ser Asp Val Thr Leu Ile Glu Gly Val Gly Asn Glu Val
 1 5 10 15
 Met Val Val Ala Gly Val Val Val Leu Ile Leu Ala Leu Val Leu Ala
 20 25 30
 Trp Leu Ser Thr Tyr Val Ala Asp Ser Gly Ser Asn Gln Leu Leu Gly
 35 40 45
 Ala Ile Val Ser Ala Gly Asp Thr Ser Val Leu His Leu Gly His Val
 50 55 60
 Asp His Leu Val Ala Gly Gln Gly Asn Pro Glu Pro Thr Glu Leu Pro
 65 70 75 80
 His Pro Ser Glu Ala Asn Thr Ser Leu Asp Lys Lys Ala Arg
 85 90

<210> 38
 <211> 218
 <212> PRT
 <213> Homo sapiens
 <400> 38
 Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met
 1 5 10 15
 Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe
 20 25 30
 Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro
 35 40 45
 Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu
 50 55 60

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Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe Ala Leu
 65 70 75 80
 Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr Ile Gly
 85 90 95
 Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr Ser Arg
 100 105 110
 Thr Val Ala Ile Ile Gly Gly Leu Ser Cys Val Gly Gln Arg Cys Trp
 115 120 125
 Gly Ala Val Pro Pro Glu Thr Ser Gln Pro Leu Pro Ala Val His Arg
 130 135 140
 Pro Gly Val Pro Gly Tyr Leu Pro His Leu Cys Gly Leu Leu Thr Ala
 145 150 155 160
 Ala Gln Gln Gly Gly Pro Ala Gly Val Ser Glu Pro Ser Pro Arg Arg
 165 170 175
 Gly Ala Asp Asp Pro Ala Val Leu Arg Ala Val Trp His Pro Gly Pro
 180 185 190
 Gly Leu Ser Val Arg Leu Leu Arg Asp Pro Arg Cys Pro Asp Pro Gly
 195 200 205
 Cys Thr Ala Ala Pro Cys His Ala Ala His
 210 215

<210> 39

<211> 460

<212> PRT

<213> Homo sapiens

<400> 39

Met Phe Thr Ile Lys Leu Leu Leu Phe Ile Val Pro Leu Val Ile Ser
 1 5 10 15
 Ser Arg Ile Asp Gln Asp Asn Ser Ser Phe Asp Ser Leu Ser Pro Glu
 20 25 30
 Pro Lys Ser Arg Phe Ala Met Leu Asp Asp Val Lys Ile Leu Ala Asn
 35 40 45
 Gly Leu Leu Gln Leu Gly His Gly Leu Lys Asp Phe Val His Lys Thr
 50 55 60
 Lys Gly Gln Ile Asn Asp Ile Phe Gln Lys Leu Asn Ile Phe Asp Gln

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65	70	75	80
Ser Phe Tyr Asp Leu Ser Leu Gln Thr	Ser Glu Ile Lys Glu Glu Glu		
85	90	95	
Lys Glu Leu Arg Arg Thr Thr Tyr Lys Leu Gln Val Lys Asn Glu Glu			
100	105	110	
Val Lys Asn Met Ser Leu Glu Leu Asn Ser Lys Leu Glu Ser Leu Leu			
115	120	125	
Glu Glu Lys Ile Leu Leu Gln Gln Lys Val Lys Tyr Leu Glu Glu Gln			
130	135	140	
Leu Thr Asn Leu Ile Gln Asn Gln Pro Glu Thr Pro Glu His Pro Glu			
145	150	155	160
Val Thr Ser Leu Lys Thr Phe Val Glu Lys Gln Asp Asn Ser Ile Lys			
165	170	175	
Asp Leu Leu Gln Thr Val Glu Asp Gln Tyr Lys Gln Leu Asn Gln Gln			
180	185	190	
His Ser Gln Ile Lys Glu Ile Glu Asn Gln Leu Arg Arg Thr Ser Ile			
195	200	205	
Gln Glu Pro Thr Glu Ile Ser Leu Ser Ser Lys Pro Arg Ala Pro Arg			
210	215	220	
Thr Thr Pro Phe Leu Gln Leu Asn Glu Ile Arg Asn Val Lys His Asp			
225	230	235	240
Gly Ile Pro Ala Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu His Thr			
245	250	255	
Ser Gly Met Tyr Ala Ile Arg Pro Ser Asn Ser Gln Val Phe His Val			
260	265	270	
Tyr Cys Asp Val Ile Ser Gly Ser Pro Trp Thr Leu Ile Gln His Arg			
275	280	285	
Ile Asp Gly Ser Gln Asn Phe Asn Glu Thr Trp Glu Asn Tyr Lys Tyr			
290	295	300	
Gly Phe Gly Arg Leu Asp Gly Glu Phe Trp Leu Gly Leu Glu Lys Ile			
305	310	315	320
Tyr Ser Ile Val Lys Gln Ser Asn Tyr Val Leu Arg Ile Glu Leu Glu			
325	330	335	
Asp Trp Lys Asp Asn Lys His Tyr Ile Glu Tyr Ser Phe Tyr Leu Gly			
340	345	350	

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Asn His Glu Thr Asn Tyr Thr Leu His Leu Val Ala Ile Thr Gly Asn
 355 360 365
 Val Pro Asn Ala Ile Pro Glu Asn Lys Asp Leu Val Phe Ser Thr Trp
 370 375 380
 Asp His Lys Ala Lys Gly His Phe Asn Cys Pro Glu Gly Tyr Ser Gly
 385 390 395 400
 Gly Trp Trp Trp His Asp Glu Cys Gly Glu Asn Asn Leu Asn Gly Lys
 405 410 415
 Tyr Asn Lys Pro Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg Gly Leu
 420 425 430
 Ser Trp Lys Ser Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser Thr Lys
 435 440 445
 Met Leu Ile His Pro Thr Asp Ser Glu Ser Phe Glu
 450 455 460

<210> 40

<211> 216

<212> PRT

<213> Homo sapiens

<400> 40

Met Val Pro Met His Leu Leu Gly Arg Leu Glu Lys Pro Leu Leu Leu
 1 5 10 15
 Leu Cys Cys Ala Ser Phe Leu Leu Gly Leu Ala Leu Leu Gly Ile Lys
 20 25 30
 Thr Asp Ile Thr Pro Val Ala Tyr Phe Phe Leu Thr Leu Gly Gly Phe
 35 40 45
 Phe Leu Phe Ala Tyr Leu Leu Val Arg Phe Leu Glu Trp Gly Leu Arg
 50 55 60
 Ser Gln Leu Gln Ser Met Gln Thr Glu Ser Pro Gly Pro Ser Gly Asn
 65 70 75 80
 Ala Arg Asp Asn Glu Ala Phe Glu Val Pro Val Tyr Glu Glu Ala Val
 85 90 95
 Val Gly Leu Glu Ser Gln Cys Arg Pro Gln Glu Leu Asp Gln Pro Pro
 100 105 110
 Pro Tyr Ser Thr Val Val Ile Pro Pro Ala Pro Glu Glu Glu Gln Pro

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115	120	125
Ser His Pro Glu Gly Ser Arg Arg Ala Lys Leu Glu Gln Arg Arg Met		
130	135	140
Ala Ser Glu Gly Ser Met Ala Gln Glu Gly Ser Pro Gly Arg Ala Pro		
145	150	155
Ile Asn Leu Arg Leu Arg Gly Pro Arg Ala Val Ser Thr Ala Pro Asp		
165	170	175
Leu Gln Ser Leu Ala Ala Val Pro Thr Leu Glu Pro Leu Thr Pro Pro		
180	185	190
Pro Ala Tyr Asp Val Cys Phe Gly His Pro Asp Asp Asp Ser Val Phe		
195	200	205
Tyr Glu Asp Asn Trp Ala Pro Pro		
210	215	

<210> 41

<211> 4335

<212> DNA

<213> Homo sapiens

<400> 41

atgcagggcc caccgctcct gaccgccgcc cacctcctct gcgtgtgcac cgccgcgctg	60
gccgtggctc ccgggcctcg gtttctggtg acagcccccag ggatcatcag gcccgaggga	120
aatgtgacta ttggggtgga gcttctggaa cactgccctt cacagggtgac tgtgaaggcg	180
gagctgctca agacagcadc aaacctcaact gtctctgtcc tggaaagcaga aggagtcttt	240
gaaaaaggct cttttaagac acttactctt ccatcactac ctctgaacag tgcagatgag	300
atztatgagc tacgtgtaac cggacgtacc caggatgaga ttttattctc taatagtacc	360
cgcttatcat ttgagaccaa gagaatatct gtcttcattc aaacagacaa ggccttatac	420
aagccaaagc aagaagtga gtttcgcatt gttacactct tctcagattt taagcettac	480
aaaacctctt taaacattct cattaaggac cccaaatcaa atttgatcca acagtgggtg	540
tcacaacaaa gtgatcttg agtcatttcc aaaacttttc agctatcttc ccatccaata	600
cttggtgact ggtctattca agttcaagtg aatgaccaga catattatca atcatttcag	660
gtttcagaat atgtattacc aaaatttgaa gtgactttgc agacaccatt atattgttct	720
atgaattcta agcattttaa tgggtaccac acggcaaagt atacatatgg gaagccagtg	780
aaaggagacg taacgcttac atttttacct ttatcctttt ggggaaagaa gaaaaatatt	840
acaaaaacat ttaagataaa tggatctgca aactctctct ttaatgatga agagatgaaa	900
aatgtaatgg attcttcaaa tggactttct gaatacctgg atctatcttt ccctggacca	960

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gtagaaattt taaccacagt gacagaatca gttacaggta tttcaagaaa tgtaagcact	1020
aatgtgttct tcaagcaaca tgattacatc attgagtttt ttgattatac tactgtcttg	1080
aagccatctc tcaacttcac agccactgtg aaggtaaactc gtgctgatgg caaccaactg	1140
actcttgaag aaagaagaaa taatgtagtc ataacagtga cacagagaaa ctatactgag	1200
tactggagcg gatctaacag tggaaatcag aaaatggaag ctgttcagaa aataaattat	1260
actgtccccc aaagtggaaac ttttaagatt gaattcccaa tcctggagga ttccagtga	1320
ctacagttga aggcctatct ccttggtagt aaaagtagca tggcagttca tagtctgttt	1380
aagtctccta gtaagacata catccaacta aaaacaagag atgaaaatat aaaggtggga	1440
tcgccttttg agttggtggt tagtggcaac aaacgattga aggagttaag ctatatggta	1500
gtatccaggg gacagttggt ggctgtagga aaacaaaatt caacaatgtt ctctttaaca	1560
ccagaaaatt cttggactcc aaaagcctgt gtaattgtgt attatattga agatgatggg	1620
gaaattataa gtgatgttct aaaaattcct gttcagcttg tttttaaaaa taagataaag	1680
ctatatggga gtaaagtga agctgaacca tctgagaaag tctctcttag gatctctgtg	1740
acacagcctg actccatagt tgggattgta gctgttgaca aaagtgtgaa tctgatgaat	1800
gcctctaattg atattacaat ggaaaatgtg gtccatgagt tggaaactta taacacagga	1860
tattatttag gcatgttcat gaattctttt gcagtccttc aggaatgtgg actctgggta	1920
ttgacagatg caaacotcac gaaggattat attgatgggtg tttatgacaa tgcagaatat	1980
gctgagaggt ttatggagga aaatgaagga catattgtag atattcatga cttttctttg	2040
ggtagcagtc cacatgtccg aaagcatttt ccagagactt ggatttggt agacaccaac	2100
atgggttcca ggatttacca agaatttgaa gtaaactgtac ctgattctat cacttcttg	2160
gtggctactg gttttgtgat ctctgaggac ctgggtcttg gactaacaac tactccagt	2220
gagctccaag ccttccaacc attttctcatt tttttgaatc ttccctactc tgttatcaga	2280
ggtgaagaat ttgctttgga aataactata ttcaattatt tgaagatgc cactgaggtt	2340
aaggtaatca ttgagaaaag tgacaaattt gatattctaa tgacttcaag tgaataaat	2400
gccacaggcc accagcagac ccttctgggt cccagtgaag atggggcaac tgttctttt	2460
cccatcaggc caacacatct gggagaaatt cctatcacag tcacagctct ttcacccact	2520
gcttctgatg ctatcaccca gatgatttta gtaaaggctg aaggaataga aaaatcatat	2580
tcacaatcca tcttattaga cttgactgac aataggctac agagtacct gaaaactttg	2640
agtttctcat ttccctctaa tacagtgaact ggcagtgaag gagttcagat cactgcaatt	2700
ggagatgttc ttggtccttc catcaatggc tttagcctcat tgattcggat gccttatggc	2760
tgtggtgaac agaacatgat aaattttgct ccaaatattt acattttgga ttatctgact	2820
aaaaagaaac aactgacaga taatttgaaa gaaaaagctc tttcatttat gaggcaaggt	2880
taccagagag aacttctcta tcagagggaa gatggctctt tcagtgcctt tgggaattat	2940
gaccttctg ggagcacttg gttgtcagct tttgttttaa gatgttctt tgaagccgat	3000
ccttacatag atattgatca gaatgtgtta cacagaacat acacttggct taaaggacat	3060

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cagaaatcca acggtgaatt ttgggatcca ggaagagtga ttcatagtga gtttcaaggt 3120
 ggcaataaaa gtccagtaac acttacagcc tatattgtaa cttctctcct gggatataga 3180
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<210> 42

<211> 1746

<212> DNA

<213> Homo sapiens

<400> 42

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70/233

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<210> 43

<211> 1230

<212> DNA

<213> Homo sapiens

<400> 43

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cttcgcagat	tcgtagtgcg	gaccatgtgt	gcggtgctag	ggctcgtggc	ccggcaggag	240
gactccggac	tcgggatca	cagtgtcagg	gtcctcattt	ccaaccatgt	gacaccttcc	300
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71/233

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<210> 44

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 44

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catgaaattc tttcagtagc tgaagttaca acttgtaat atgaagttgt cattttgaca 720
ccactcttgt gcagtcaccc taaatatagg ttcagagcat ctctgtgaa tgacatattt 780
tgtcaatcac tgccaggatc tccatttaag cccctcacc tgaggcagct ggagcagcag 840

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72/233

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<210> 45

<211> 1821

<212> DNA

<213> Homo sapiens

<400> 45

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73/233

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cccatgaagc aggtccagaa c 1821

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<210> 46

<211> 942

<212> DNA

<213> Homo sapiens

<400> 46

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gtgaagctgt ctgcacctgt cacctacact aaacacatcc agcccatctg tctccaggcc 480
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ggctgtggtc ggcccaatcg gcccggtgtc tacaccaata tcagccacca ctttgagtgg 840
atccagaagc tgatggccca gagtggcatg tccagccag accctcctg gccgctactc 900
ttttccctc ttctctgggc tctcccactc ctggggcgcg tc 942

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74/233

<210> 47

<211> 282

<212> DNA

<213> Homo sapiens

<400> 47

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agcggtagca accagctcct gggcgtatt gtgtcagcag gcgacacatc cgtcctccac	180
ctggggcatg tggaccacct ggtggcaggc caaggcaacc ccgagccaac tgaactcccc	240
catccatcag aggcaaatac ttccctggac aagaaagcca ga	282

<210> 48

<211> 654

<212> DNA

<213> Homo sapiens

<400> 48

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<210> 49

<211> 1380

<212> DNA

<213> Homo sapiens

<400> 49

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75/233

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gtccataaga cgaagggcca aattaatgac atatttcaaa aactcaacat atttgatcag	240
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<210> 50

<211> 648

<212> DNA

<213> Homo sapiens

<400> 50

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ttctttctca cattgggtgg cttctctttg ttgctctatc tctgggtccg gttttggaa	180
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ccagcacctg aggaggaaca acctagccat ccagaggggt ccaggagagc caaactggaa	420

76/233

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 ggggcagtcc ccacattaga gcctctgact ccacccctg cctatgatgt ctgctttggt 600
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<210> 51

<211> 4473

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (45)...(4382)

<400> 51

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1

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 Pro Leu Leu Thr Ala Ala His Leu Leu Cys Val Cys Thr Ala Ala Leu
 5 10 15 20

gcc gtg got ccc ggg cct cgg ttt ctg gtg aca gcc cca ggg atc atc 152
 Ala Val Ala Pro Gly Pro Arg Phe Leu Val Thr Ala Pro Gly Ile Ile
 25 30 35

agg ccc gga gga aat gtg act att ggg gtg gag ctt ctg gaa cac tgc 200
 Arg Pro Gly Gly Asn Val Thr Ile Gly Val Glu Leu Leu Glu His Cys
 40 45 50

cct tca cag gtg act gtg aag gcg gag ctg ctc aag aca gca tca aac 248
 Pro Ser Gln Val Thr Val Lys Ala Glu Leu Leu Lys Thr Ala Ser Asn
 55 60 65

ctc act gtc tct gtc ctg gaa gca gaa gga gtc ttt gaa aaa ggc tct 296
 Leu Thr Val Ser Val Leu Glu Ala Glu Gly Val Phe Glu Lys Gly Ser
 70 75 80

ttt aag aca ctt act ctt cca tca cta cct ctg aac agt gca gat gag 344
 Phe Lys Thr Leu Thr Leu Pro Ser Leu Pro Leu Asn Ser Ala Asp Glu
 85 90 95 100

att tat gag cta cgt gta acc gga cgt acc cag gat gag att tta ttc 392

77/233

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Ser Asn Ser Thr Arg Leu Ser Phe Glu Thr Lys Arg Ile Ser Val Phe	
120 125 130	
att caa aca gac aag gcc tta tac aag cca aag caa gaa gtg aag ttt	488
Ile Gln Thr Asp Lys Ala Leu Tyr Lys Pro Lys Gln Glu Val Lys Phe	
135 140 145	
cgc att gtt aca ctc ttc tca gat ttt aag cct tac aaa acc tct tta	536
Arg Ile Val Thr Leu Phe Ser Asp Phe Lys Pro Tyr Lys Thr Ser Leu	
150 155 160	
aac att ctc att aag gac ccc aaa tca aat ttg atc caa cag tgg ttg	584
Asn Ile Leu Ile Lys Asp Pro Lys Ser Asn Leu Ile Gln Gln Trp Leu	
165 170 175 180	
tca caa caa agt gat ctt gga gtc att tcc aaa act ttt cag cta tct	632
Ser Gln Gln Ser Asp Leu Gly Val Ile Ser Lys Thr Phe Gln Leu Ser	
185 190 195	
tcc cat cca ata ctt ggt gac tgg tct att caa gtt caa gtg aat gac	680
Ser His Pro Ile Leu Gly Asp Trp Ser Ile Gln Val Gln Val Asn Asp	
200 205 210	
cag aca tat tat caa tca ttt cag gtt tca gaa tat gta tta cca aaa	728
Gln Thr Tyr Tyr Gln Ser Phe Gln Val Ser Glu Tyr Val Leu Pro Lys	
215 220 225	
ttt gaa gtg act ttg cag aca cca tta tat tgt tct atg aat tct aag	776
Phe Glu Val Thr Leu Gln Thr Pro Leu Tyr Cys Ser Met Asn Ser Lys	
230 235 240	
cat tta aat ggt acc atc acg gca aag tat aca tat ggg aag cca gtg	824
His Leu Asn Gly Thr Ile Thr Ala Lys Tyr Thr Tyr Gly Lys Pro Val	
245 250 255 260	
aaa gga gac gta acg ctt aca ttt tta cct tta tcc ttt tgg gga aag	872
Lys Gly Asp Val Thr Leu Thr Phe Leu Pro Leu Ser Phe Trp Gly Lys	
265 270 275	
aag aaa aat att aca aaa aca ttt aag ata aat gga tct gca aac ttc	920
Lys Lys Asn Ile Thr Lys Thr Phe Lys Ile Asn Gly Ser Ala Asn Phe	
280 285 290	

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tct ttt aat gat gaa gag atg aaa aat gta atg gat tct tca aat gga	968
Ser Phe Asn Asp Glu Glu Met Lys Asn Val Met Asp Ser Ser Asn Gly	
295 300 305	
ott tct gaa tac ctg gat cta tct ttc cct gga cca gta gaa att tta	1016
Leu Ser Glu Tyr Leu Asp Leu Ser Phe Pro Gly Pro Val Glu Ile Leu	
310 315 320	
acc aca gtg aca gaa tca gtt aca ggt att tca aga aat gta agc act	1064
Thr Thr Val Thr Glu Ser Val Thr Gly Ile Ser Arg Asn Val Ser Thr	
325 330 335 340	
aat gtg ttc ttc aag caa cat gat tac atc att gag ttt ttt gat tat	1112
Asn Val Phe Phe Lys Gln His Asp Tyr Ile Ile Glu Phe Phe Asp Tyr	
345 350 355	
act act gtc ttg aag cca tct ctc aac ttc aca gcc act gtg aag gta	1160
Thr Thr Val Leu Lys Pro Ser Leu Asn Phe Thr Ala Thr Val Lys Val	
360 365 370	
act cgt gct gat ggc aac caa ctg act ctt gaa gaa aga aga aat aat	1208
Thr Arg Ala Asp Gly Asn Gln Leu Thr Leu Glu Glu Arg Arg Asn Asn	
375 380 385	
gta gtc ata aca gtg aca cag aga aac tat act gag tac tgg agc gga	1256
Val Val Ile Thr Val Thr Gln Arg Asn Tyr Thr Glu Tyr Trp Ser Gly	
390 395 400	
tct aac agt gga aat cag aaa atg gaa gct gtt cag aaa ata aat tat	1304
Ser Asn Ser Gly Asn Gln Lys Met Glu Ala Val Gln Lys Ile Asn Tyr	
405 410 415 420	
act gtc ccc caa agt gga act ttt aag att gaa ttc cca atc ctg gag	1352
Thr Val Pro Gln Ser Gly Thr Phe Lys Ile Glu Phe Pro Ile Leu Glu	
425 430 435	
gat tcc agt gag cta cag ttg aag gcc tat ttc ctt ggt agt aaa agt	1400
Asp Ser Ser Glu Leu Gln Leu Lys Ala Tyr Phe Leu Gly Ser Lys Ser	
440 445 450	
agc atg gca gtt cat agt ctg ttt aag tct cct agt aag aca tac atc	1448
Ser Met Ala Val His Ser Leu Phe Lys Ser Pro Ser Lys Thr Tyr Ile	
455 460 465	
caa cta aaa aca aga gat gaa aat ata aag gtg gga tcg cct ttt gag	1496
Gln Leu Lys Thr Arg Asp Glu Asn Ile Lys Val Gly Ser Pro Phe Glu	

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470	475	480	
ttg gtg gtt agt ggc aac aaa cga ttg aag gag tta agc tat atg gta			1544
Leu Val Val Ser Gly Asn Lys Arg Leu Lys Glu Leu Ser Tyr Met Val			
485	490	495	500
gta tcc agg gga cag ttg gtg gct gta gga aaa caa aat tca aca atg			1592
Val Ser Arg Gly Gln Leu Val Ala Val Gly Lys Gln Asn Ser Thr Met			
505	510	515	
ttc tct tta aca cca gaa aat tct tgg act cca aaa gcc tgt gta att			1640
Phe Ser Leu Thr Pro Glu Asn Ser Trp Thr Pro Lys Ala Cys Val Ile			
520	525	530	
gtg tat tat att gaa gat gat ggg gaa att ata agt gat gtt cta aaa			1688
Val Tyr Tyr Ile Glu Asp Asp Gly Glu Ile Ile Ser Asp Val Leu Lys			
535	540	545	
att cct gtt cag ctt gtt ttt aaa aat aag ata aag cta tat tgg agt			1736
Ile Pro Val Gln Leu Val Phe Lys Asn Lys Ile Lys Leu Tyr Trp Ser			
550	555	560	
aaa gtg aaa gct gaa cca tct gag aaa gtc tct ctt agg atc tct gtg			1784
Lys Val Lys Ala Glu Pro Ser Glu Lys Val Ser Leu Arg Ile Ser Val			
565	570	575	580
aca cag cct gac tcc ata gtt ggg att gta gct gtt gac aaa agt gtg			1832
Thr Gln Pro Asp Ser Ile Val Gly Ile Val Ala Val Asp Lys Ser Val			
585	590	595	
aat ctg atg aat gcc tct aat gat att aca atg gaa aat gtg gtc cat			1880
Asn Leu Met Asn Ala Ser Asn Asp Ile Thr Met Glu Asn Val Val His			
600	605	610	
gag ttg gaa ctt tat aac aca gga tat tat tta ggc atg ttc atg aat			1928
Glu Leu Glu Leu Tyr Asn Thr Gly Tyr Tyr Leu Gly Met Phe Met Asn			
615	620	625	
tct ttt gca gtc ttt cag gaa tgt gga ctc tgg gta ttg aca gat gca			1976
Ser Phe Ala Val Phe Gln Glu Cys Gly Leu Trp Val Leu Thr Asp Ala			
630	635	640	
aac ctc acg aag gat tat att gat ggt gtt tat gac aat gca gaa tat			2024
Asn Leu Thr Lys Asp Tyr Ile Asp Gly Val Tyr Asp Asn Ala Glu Tyr			
645	650	655	660
gct gag agg ttt atg gag gaa aat gaa gga cat att gta gat att cat			2072

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Ala Glu Arg Phe Met Glu Glu Asn Glu Gly His Ile Val Asp Ile His	
665 670 675	
gac ttt tct ttg ggt agc agt cca cat gtc cga aag cat ttt cca gag	2120
Asp Phe Ser Leu Gly Ser Ser Pro His Val Arg Lys His Phe Pro Glu	
680 685 690	
act tgg att tgg cta gac acc aac atg ggt tcc agg att tac caa gaa	2168
Thr Trp Ile Trp Leu Asp Thr Asn Met Gly Ser Arg Ile Tyr Gln Glu	
695 700 705	
ttt gaa gta act gta cct gat tct atc act tct tgg gtg gct act ggt	2216
Phe Glu Val Thr Val Pro Asp Ser Ile Thr Ser Trp Val Ala Thr Gly	
710 715 720	
ttt gtg atc tct gag gac ctg ggt ctt gga cta aca act act cca gtg	2264
Phe Val Ile Ser Glu Asp Leu Gly Leu Gly Leu Thr Thr Thr Pro Val	
725 730 735 740	
gag ctg caa gcc ttc caa cca ttt ttc att ttt ttg aat ctt ccc tac	2312
Glu Leu Gln Ala Phe Gln Pro Phe Phe Ile Phe Leu Asn Leu Pro Tyr	
745 750 755	
tct gtt atc aga ggt gaa gaa ttt gct ttg gaa ata act ata ttc aat	2360
Ser Val Ile Arg Gly Glu Glu Phe Ala Leu Glu Ile Thr Ile Phe Asn	
760 765 770	
tat ttg aaa gat gcc act gag gtt aag gta atc att gag aaa agt gac	2408
Tyr Leu Lys Asp Ala Thr Glu Val Lys Val Ile Ile Glu Lys Ser Asp	
775 780 785	
aaa ttt gat att cta atg act tca agt gaa ata aat gcc aca ggc cac	2456
Lys Phe Asp Ile Leu Met Thr Ser Ser Glu Ile Asn Ala Thr Gly His	
790 795 800	
cag cag acc ctt ctg gtt ccc agt gag gat ggg gca act gtt ctt ttt	2504
Gln Gln Thr Leu Leu Val Pro Ser Glu Asp Gly Ala Thr Val Leu Phe	
805 810 815 820	
ccc atc agg cca aca cat ctg gga gaa att cct atc aca gtc aca gct	2552
Pro Ile Arg Pro Thr His Leu Gly Glu Ile Pro Ile Thr Val Thr Ala	
825 830 835	
ctt tca ccc act gct tct gat gct atc acc cag atg att tta gta aag	2600
Leu Ser Pro Thr Ala Ser Asp Ala Ile Thr Gln Met Ile Leu Val Lys	
840 845 850	

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gct gaa gga ata gaa aaa tca tat tca caa tcc atc tta tta gac ttg	2648
Ala Glu Gly Ile Glu Lys Ser Tyr Ser Gln Ser Ile Leu Leu Asp Leu	
855 860 865	
act gac aat agg cta cag agt acc ctg aaa act ttg agt ttc tca ttt	2696
Thr Asp Asn Arg Leu Gln Ser Thr Leu Lys Thr Leu Ser Phe Ser Phe	
870 875 880	
cct cct aat aca gtg act ggc agt gaa aga gtt cag atc act gca att	2744
Pro Pro Asn Thr Val Thr Gly Ser Glu Arg Val Gln Ile Thr Ala Ile	
885 890 895 900	
gga gat gtt ctt ggt cct tcc atc aat ggc tta gcc tca ttg att cgg	2792
Gly Asp Val Leu Gly Pro Ser Ile Asn Gly Leu Ala Ser Leu Ile Arg	
905 910 915	
atg cct tat ggc tgt ggt gaa cag aac atg ata aat ttt gct cca aat	2840
Met Pro Tyr Gly Cys Gly Glu Gln Asn Met Ile Asn Phe Ala Pro Asn	
920 925 930	
att tac att ttg gat tat ctg act aaa aag aaa caa ctg aca gat aat	2888
Ile Tyr Ile Leu Asp Tyr Leu Thr Lys Lys Lys Gln Leu Thr Asp Asn	
935 940 945	
ttg aaa gaa aaa gct ctt tca ttt atg agg caa ggt tac cag aga gaa	2936
Leu Lys Glu Lys Ala Leu Ser Phe Met Arg Gln Gly Tyr Gln Arg Glu	
950 955 960	
ctt ctc tat cag agg gaa gat ggc tct ttc agt gct ttt ggg aat tat	2984
Leu Leu Tyr Gln Arg Glu Asp Gly Ser Phe Ser Ala Phe Gly Asn Tyr	
965 970 975 980	
gac cct tct ggg agc act tgg ttg tca gct ttt gtt tta aga tgt ttc	3032
Asp Pro Ser Gly Ser Thr Trp Leu Ser Ala Phe Val Leu Arg Cys Phe	
985 990 995	
ctt gaa gcc gat cct tac ata gat att gat cag aat gtg tta cac aga	3080
Leu Glu Ala Asp Pro Tyr Ile Asp Ile Asp Gln Asn Val Leu His Arg	
1000 1005 1010	
aca tac act tgg ctt aaa gga cat cag aaa tcc aac ggt gaa ttt tgg	3128
Thr Tyr Thr Trp Leu Lys Gly His Gln Lys Ser Asn Gly Glu Phe Trp	
1015 1020 1025	
gat cca gga aga gtg att cat agt gag ctt caa ggt ggc aat aaa agt	3176
Asp Pro Gly Arg Val Ile His Ser Glu Leu Gln Gly Gly Asn Lys Ser	

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1030	1035	1040	
cca gta aca ctt aca gcc tat att gta act tct ctc ctg gga tat aga			3224
Pro Val Thr Leu Thr Ala Tyr Ile Val Thr Ser Leu Leu Gly Tyr Arg			
1045	1050	1055	1060
aag tat cag cct aac att gat gtg caa gag tct atc cat ttt ttg gag			3272
Lys Tyr Gln Pro Asn Ile Asp Val Gln Glu Ser Ile His Phe Leu Glu			
1065	1070	1075	
tct gaa ttc agt aga gga att tca gac aat tat act cta gcc ctt ata			3320
Ser Glu Phe Ser Arg Gly Ile Ser Asp Asn Tyr Thr Leu Ala Leu Ile			
1080	1085	1090	
act tat gca ttg tca tca gtg ggg agt cct aaa gcg aag gaa gct ttg			3368
Thr Tyr Ala Leu Ser Ser Val Gly Ser Pro Lys Ala Lys Glu Ala Leu			
1095	1100	1105	
aat atg ctg act tgg aga gca gaa caa gaa ggt ggc atg caa ttc tgg			3416
Asn Met Leu Thr Trp Arg Ala Glu Gln Glu Gly Gly Met Gln Phe Trp			
1110	1115	1120	
gtg tca tca gag tcc aaa ctt tct gac tcc tgg cag cca cgc tcc ctg			3464
Val Ser Ser Glu Ser Lys Leu Ser Asp Ser Trp Gln Pro Arg Ser Leu			
1125	1130	1135	1140
gat att gaa gtt gca gcc tat gca ctg ctc tca cac ttc tta caa ttt			3512
Asp Ile Glu Val Ala Ala Tyr Ala Leu Leu Ser His Phe Leu Gln Phe			
1145	1150	1155	
cag act tct gag gga atc cca att atg agg tgg cta agc agg caa aga			3560
Gln Thr Ser Glu Gly Ile Pro Ile Met Arg Trp Leu Ser Arg Gln Arg			
1160	1165	1170	
aat agc ttg ggt ggt ttt gca tct act cag gat acc act gtg gct tta			3608
Asn Ser Leu Gly Gly Phe Ala Ser Thr Gln Asp Thr Thr Val Ala Leu			
1175	1180	1185	
aag gct ctg tct gaa ttt gca gcc cta atg aat aca gaa agg aca aat			3656
Lys Ala Leu Ser Glu Phe Ala Ala Leu Met Asn Thr Glu Arg Thr Asn			
1190	1195	1200	
atc caa gtg acc gtg acg ggg cct agc tca cca agt cct gta aag ttt			3704
Ile Gln Val Thr Val Thr Gly Pro Ser Ser Pro Ser Pro Val Lys Phe			
1205	1210	1215	1220
ctg att gac aca cac aac cgc tta ctc ctt cag aca gca gag ctt gct			3752

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Leu Ile Asp Thr His Asn Arg Leu Leu Leu Gln Thr Ala Glu Leu Ala	
1225 1230 1235	
gtg gta cag cca acg gca gtt aat att tcc gca aat ggt ttt gga ttt	3800
Val Val Gln Pro Thr Ala Val Asn Ile Ser Ala Asn Gly Phe Gly Phe	
1240 1245 1250	
gct att tgt cag ctc aat gtt gta tat aat gtg aag gct tct ggg tct	3848
Ala Ile Cys Gln Leu Asn Val Val Tyr Asn Val Lys Ala Ser Gly Ser	
1255 1260 1265	
tct aga aga cga aga tct atc caa aat caa gaa gcc ttt gat tta gat	3896
Ser Arg Arg Arg Arg Ser Ile Gln Asn Gln Glu Ala Phe Asp Leu Asp	
1270 1275 1280	
gtt gct gta aaa gaa aat aaa gat gat ctc aat cat gtg gat ttg aat	3944
Val Ala Val Lys Glu Asn Lys Asp Asp Leu Asn His Val Asp Leu Asn	
1285 1290 1295 1300	
gtg tgt aca agc ttt tcg ggc ccg ggt agg agt ggc atg gct ctt atg	3992
Val Cys Thr Ser Phe Ser Gly Pro Gly Arg Ser Gly Met Ala Leu Met	
1305 1310 1315	
gaa gtt aac cta tta agt ggc ttt atg gtg cct tca gaa gca att tct	4040
Glu Val Asn Leu Leu Ser Gly Phe Met Val Pro Ser Glu Ala Ile Ser	
1320 1325 1330	
ctg agc gag aca gtg aag aaa gtg gaa tat gat cat gga aaa ctc aac	4088
Leu Ser Glu Thr Val Lys Lys Val Glu Tyr Asp His Gly Lys Leu Asn	
1335 1340 1345	
ctc tat tta gat tct gta aat gaa acc cag ttt tgt gtt aat att cct	4136
Leu Tyr Leu Asp Ser Val Asn Glu Thr Gln Phe Cys Val Asn Ile Pro	
1350 1355 1360	
gct gtg aga aac ttt aaa gtt tca aat acc caa gat gct tca gtg tcc	4184
Ala Val Arg Asn Phe Lys Val Ser Asn Thr Gln Asp Ala Ser Val Ser	
1365 1370 1375 1380	
ata gtg gat tac tat gag cca agg aga cag gcg gtg aga agt tac aac	4232
Ile Val Asp Tyr Tyr Glu Pro Arg Arg Gln Ala Val Arg Ser Tyr Asn	
1385 1390 1395	
tct gaa gtg aag ctg tcc tcc tgt gac ctt tgc agt gat gtc cag ggc	4280
Ser Glu Val Lys Leu Ser Ser Cys Asp Leu Cys Ser Asp Val Gln Gly	
1400 1405 1410	

tgc cgt cct tgt gag gat gga gct tca ggc tcc cat cat cac tct tca	4328
Cys Arg Pro Cys Glu Asp Gly Ala Ser Gly Ser His His His Ser Ser	
1415 1420 1425	
gtc att ttt att ttc tgt ttc aag ctt ctg tac ttt atg gaa ctt tgg	4376
Val Ile Phe Ile Phe Cys Phe Lys Leu Leu Tyr Phe Met Glu Leu Trp	
1430 1435 1440	
ctg tgatttatatt ttaaaggact ctgtgtaaca ctaacatttc cagtagtcac a	4430
Leu	
1445	
tggtgattggtt ttgttttcgt agaagaatac tgcttctatt ttg	4473

agttctggga	ggcgggggga	aggaggttgg	tggcgactcc	ctcgtctgcc	ctcactgccg	60										
gcggtcccaa	ctccaggcac	c	atg	ttc	ccc	gcg	ggc	ccc	ccc	agc	cac	agc	111			
		Met	Phe	Pro	Ala	Gly	Pro	Pro	Ser	His	Ser					
		1				5						10				
ctc	ctc	cgg	ctc	ccc	ctg	ctg	cag	ttg	ctg	cta	ctg	gtg	gtg	cag	gcc	159
Leu	Leu	Arg	Leu	Pro	Leu	Leu	Gln	Leu	Leu	Leu	Leu	Val	Val	Gln	Ala	
			15					20						25		
gtg	ggg	agg	ggg	ctg	ggc	cgc	gcc	agc	ccg	gcc	ggg	ggc	ccc	ctg	gaa	207
Val	Gly	Arg	Gly	Leu	Gly	Arg	Ala	Ser	Pro	Ala	Gly	Gly	Pro	Leu	Glu	
			30					35					40			
gat	gtg	gtc	atc	gag	agg	tac	cac	atc	ccc	agg	gcc	tgt	ccc	cgg	gaa	255
Asp	Val	Val	Ile	Glu	Arg	Tyr	His	Ile	Pro	Arg	Ala	Cys	Pro	Arg	Glu	
			45					50					55			
gtg	cag	atg	ggg	gat	ttt	gtg	cgc	tac	cac	tac	aac	ggc	act	ttt	gaa	303
Val	Gln	Met	Gly	Asp	Phe	Val	Arg	Tyr	His	Tyr	Asn	Gly	Thr	Phe	Glu	
			60					65					70			

gat ggc aag aag ttt gat tca agc tat gat cgc aac acc ttg gtg gcc	351
Asp Gly Lys Lys Phe Asp Ser Ser Tyr Asp Arg Asn Thr Leu Val Ala	
75 80 85 90	
atc gtg gtg ggt gtg ggg cgc ctc atc act gcc atg gac cga gcc ctc	399
Ile Val Val Gly Val Gly Arg Leu Ile Thr Gly Met Asp Arg Gly Leu	
95 100 105	
atg gcc atg tgt gtc aac gag cgg cga cgc ctc att gtg cct ccc cac	447
Met Gly Met Cys Val Asn Glu Arg Arg Arg Leu Ile Val Pro Pro His	
110 115 120	
ctg gcc tat ggg agc atc gcc ctg gcg ggg ctc att cca ccg gat gcc	495
Leu Gly Tyr Gly Ser Ile Gly Leu Ala Gly Leu Ile Pro Pro Asp Ala	
125 130 135	
acc ctc tac ttc gat gtg gtt ctg ctg gat gtg tgg aac aag gaa gac	543
Thr Leu Tyr Phe Asp Val Val Leu Leu Asp Val Trp Asn Lys Glu Asp	
140 145 150	
acc gtg cag gtg agc aca ttg ctg cgc ccg ccc cac tgc ccc cgc atg	591
Thr Val Gln Val Ser Thr Leu Leu Arg Pro Pro His Cys Pro Arg Met	
155 160 165 170	
gtc cag gac gcc gac ttt gtc cgc tac cac tac aat gcc acc ctg ctg	639
Val Gln Asp Gly Asp Phe Val Arg Tyr His Tyr Asn Gly Thr Leu Leu	
175 180 185	
gac gcc acc tcc ttc gac acc agc tac agt aag gcc gcc act tat gac	687
Asp Gly Thr Ser Phe Asp Thr Ser Tyr Ser Lys Gly Gly Thr Tyr Asp	
190 195 200	
acc tac gtc gcc tct ggt tgg ctg atc aag gcc atg gac cag ggg ctg	735
Thr Tyr Val Gly Ser Gly Trp Leu Ile Lys Gly Met Asp Gln Gly Leu	
205 210 215	
ctg gcc atg tgt cct gga gag aga agg aag att atc atc cct cca ttc	783
Leu Gly Met Cys Pro Gly Glu Arg Arg Lys Ile Ile Ile Pro Pro Phe	
220 225 230	
ctg gcc tat gcc gag aaa gcc tat ggg acg gtg atc ccc cca cag gcc	831
Leu Ala Tyr Gly Glu Lys Gly Tyr Gly Thr Val Ile Pro Pro Gln Ala	
235 240 245 250	
tcg ctg gtc ttt cac gtc ctc ctg att gac gtg cac aac ccg aag gac	879
Ser Leu Val Phe His Val Leu Leu Ile Asp Val His Asn Pro Lys Asp	

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255	260	265	
gct gtc cag cta gag acg ctg gag ctc ccc ccc ggc tgt gtc cgc aga			927
Ala Val Gln Leu Glu Thr Leu Glu Leu Pro Pro Gly Cys Val Arg Arg			
270	275	280	
gcc ggg gcc ggg gac ttc atg cgc tac cac tac aat ggc tcc ttg atg			975
Ala Gly Ala Gly Asp Phe Met Arg Tyr His Tyr Asn Gly Ser Leu Met			
285	290	295	
gac ggc acc ctc ttc gat tcc agc tac tcc cgc aac cac acc tac aat			1023
Asp Gly Thr Leu Phe Asp Ser Ser Tyr Ser Arg Asn His Thr Tyr Asn			
300	305	310	
acc tat atc ggg cag ggt tac atc atc ccc ggg atg gac cag ggg ctg			1071
Thr Tyr Ile Gly Gln Gly Tyr Ile Ile Pro Gly Met Asp Gln Gly Leu			
315	320	325	330
cag ggt gcc tgc atg ggg gaa cgc cgg aga att acc atc ccc ccg cac			1119
Gln Gly Ala Cys Met Gly Glu Arg Arg Arg Ile Thr Ile Pro Pro His			
335	340	345	
ctc gcc tat ggg gag aat gga act gga gac aag atc cct ggc tot gcc			1167
Leu Ala Tyr Gly Glu Asn Gly Thr Gly Asp Lys Ile Pro Gly Ser Ala			
350	355	360	
gtg cta atc ttc aac gtc cat gtc att gac ttc cac aac cct gcg gat			1215
Val Leu Ile Phe Asn Val His Val Ile Asp Phe His Asn Pro Ala Asp			
365	370	375	
gtg gtg gaa atc agg aca ctg tcc cgg cca tot gag acc tgc aat gag			1263
Val Val Glu Ile Arg Thr Leu Ser Arg Pro Ser Glu Thr Cys Asn Glu			
380	385	390	
acc acc aag ctt ggg gac ttt gtt cga tac cat tac aac tgt tot ttg			1311
Thr Thr Lys Leu Gly Asp Phe Val Arg Tyr His Tyr Asn Cys Ser Leu			
395	400	405	410
ctg gac ggc acc cag ctg ttc acc tcg cat gac tac ggg gcc ccc cag			1359
Leu Asp Gly Thr Gln Leu Phe Thr Ser His Asp Tyr Gly Ala Pro Gln			
415	420	425	
gag gcg act ctc ggg gcc aac aag gtg atc gaa ggc ctg gac acg ggc			1407
Glu Ala Thr Leu Gly Ala Asn Lys Val Ile Glu Gly Leu Asp Thr Gly			
430	435	440	
ctg cag ggc atg tgt gtg gga gag agg cgg cag ctc atc gtg ccc ccg			1455

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Leu Gln Gly Met Cys Val Gly Glu Arg Arg Gln Leu Ile Val Pro Pro
 445 450 455
 cac ctg gcc cac ggg gag agt gga gcc cgg gga gtc cca ggc agt got 1503
 His Leu Ala His Gly Glu Ser Gly Ala Arg Gly Val Pro Gly Ser Ala
 460 465 470
 gtg ctg ctg ttt gag gtg gag ctg gtg tcc cgg gag gat ggg ctg ccc 1551
 Val Leu Leu Phe Glu Val Glu Leu Val Ser Arg Glu Asp Gly Leu Pro
 475 480 485 490
 aca ggc tac ctg ttt gtg tgg cac aag gac cct cct gcc aac ctg ttt 1599
 Thr Gly Tyr Leu Phe Val Trp His Lys Asp Pro Pro Ala Asn Leu Phe
 495 500 505
 gaa gac atg gac ctc aac aag gat ggc gag gtc cct ccg gag gag ttc 1647
 Glu Asp Met Asp Leu Asn Lys Asp Gly Glu Val Pro Pro Glu Glu Phe
 510 515 520
 tcc acc ttc atc aag gct caa gtg agt gag ggc aaa gga cgc ctc atg 1695
 Ser Thr Phe Ile Lys Ala Gln Val Ser Glu Gly Lys Gly Arg Leu Met
 525 530 535
 cct ggg cag gac cct gag aaa acc ata gga gac atg ttc cag aac cag 1743
 Pro Gly Gln Asp Pro Glu Lys Thr Ile Gly Asp Met Phe Gln Asn Gln
 540 545 550
 gac cgc aac cag gac ggc aag atc aca gtc gac gag ctc aag ctg aag 1791
 Asp Arg Asn Gln Asp Gly Lys Ile Thr Val Asp Glu Leu Lys Leu Lys
 555 560 565 570
 tca gat gag gac gag gag cgg gtc cac gag gag ctc tga ggggcaggga 1840
 Ser Asp Glu Asp Glu Glu Arg Val His Glu Glu Leu
 575 580
 gcctggccag gcctgagaca cagaggccca ctgcgagggg gacagtggcg gtgggactga 1900
 cctgctgaca gtcacccctcc ctctgctggg atgaggtcca ggagccaact aaaacaatgg 1960
 cagaggagac atctctggtg tccccaccac cctagatgaa aatccacagc acagacctct 2020
 accgtgtttc tcttccatcc ctaaaocact tccctaaaat gtttgattt gcaaagccaa 2080
 tttggggcct gtggagcctg ggggttgata gggccatggc tgggtcccca ccatacctcc 2140
 cctccacatc actgacacag ctgagcttgt tatccatctc cccaaacttt ctctttcttt 2200
 gtactttctg tcatccccac tcccagcccc tattctcteta tgtgacagct ggctaggacc 2260
 cctctgcctt cctccccaat cctgactggc tcttagggaa ggggaaggct cctggagggc 2320
 agccctacct ctcccatgcc ctttgccctc ctccctcgcc tccagtggag gctgagctga 2380

88/233

ccctgggctg ctggaggcca gactgggctg tagttagctt ttcaccccta aagaaggctt 2440
 tccctaagga accatagaag agaggaagaa aacaaagggc atgtgtgagg gaagctgctt 2500
 ggggtgggtgt tagggctatg aaatcttgga tttggggctg aggggtggga gggagggcag 2560
 agctctgcac actcaaaggc taaactggtg tcagtccttt tttcctttgt tccaaataaa 2620
 agattaaacc 2630

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (89)...(1321)

<400> 53

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 acggccgggc gctcctgaag cagcagtt atg gag ctt ccc tca ggg ccg ggg 112

Met Glu Leu Pro Ser Gly Pro Gly

1

5

ccg gag cgg ctc ttt gac tcg cac cgg ctt ccg ggt gac tgc ttc cta 160
 Pro Glu Arg Leu Phe Asp Ser His Arg Leu Pro Gly Asp Cys Phe Leu

10

15

20

ctg ctc gtg ctg ctg ctc tac gcg cca gtc ggg ttc tgc ctc ctc gtc 208
 Leu Leu Val Leu Leu Leu Tyr Ala Pro Val Gly Phe Cys Leu Leu Val

25

30

35

40

ctg cgc ctc ttt ctc ggg atc cac gtc ttc ctg gtc agc tgc gcg ctg 256
 Leu Arg Leu Phe Leu Gly Ile His Val Phe Leu Val Ser Cys Ala Leu

45

50

55

cca gac agc gtc ctt cgc aga ttc gta gtg cgg acc atg tgt gcg gtg 304
 Pro Asp Ser Val Leu Arg Arg Phe Val Val Arg Thr Met Cys Ala Val

60

65

70

cta ggg ctc gtg gcc cgg cag gag gac tcc gga ctc cgg gat cac agt 352
 Leu Gly Leu Val Ala Arg Gln Glu Asp Ser Gly Leu Arg Asp His Ser

75

80

85

gtc agg gtc ctc att tcc aac cat gtg aca cct ttc gac cac aac ata 400
 Val Arg Val Leu Ile Ser Asn His Val Thr Pro Phe Asp His Asn Ile

89/233

90	95	100	
gtc aat ttg ctt acc acc tgt agc acc cct cta ctc aat agt ccc ccc			448
Val Asn Leu Leu Thr Thr Cys Ser Thr Pro Leu Leu Asn Ser Pro Pro			
105	110	115	120
agc ttt gtg tgc tgg tct cgg ggc ttc atg gag atg aat ggg cgg ggg			496
Ser Phe Val Cys Trp Ser Arg Gly Phe Met Glu Met Asn Gly Arg Gly			
125	130	135	
gag ttg gtg gag tca ctc aag aga ttc tgt gct tcc acg agg ctt ccc			544
Glu Leu Val Glu Ser Leu Lys Arg Phe Cys Ala Ser Thr Arg Leu Pro			
140	145	150	
ccc act cct ctg ctg cta ttc cct gag gaa gag gcc acc aat ggc cgg			592
Pro Thr Pro Leu Leu Leu Phe Pro Glu Glu Glu Ala Thr Asn Gly Arg			
155	160	165	
gag ggg ctc ctg cgc ttc agt tcc tgg cca ttt tct atc caa gat gtg			640
Glu Gly Leu Leu Arg Phe Ser Ser Trp Pro Phe Ser Ile Gln Asp Val			
170	175	180	
gta caa cct ctt acc ctg caa gtt cag aga ccc ctg gtc tct gtg acg			688
Val Gln Pro Leu Thr Leu Gln Val Gln Arg Pro Leu Val Ser Val Thr			
185	190	195	200
gtg tca gat gcc tcc tgg gtc tca gaa ctg ctg tgg tca ctt ttc gtc			736
Val Ser Asp Ala Ser Trp Val Ser Glu Leu Leu Trp Ser Leu Phe Val			
205	210	215	
cct ttc acg gtg tat caa gta agg tgg ctt cgt cct gtt cat cgc caa			784
Pro Phe Thr Val Tyr Gln Val Arg Trp Leu Arg Pro Val His Arg Gln			
220	225	230	
cta ggg gaa gcg aat gag gag ttt gca ctc cgt gta caa cag ctg gtg			832
Leu Gly Glu Ala Asn Glu Glu Phe Ala Leu Arg Val Gln Gln Leu Val			
235	240	245	
gcc aag gaa ttg ggc cag aca ggg aca cgg ctc act cca gct gac aaa			880
Ala Lys Glu Leu Gly Gln Thr Gly Thr Arg Leu Thr Pro Ala Asp Lys			
250	255	260	
gca gag cac atg aag cga caa aga cac ccc aga ttg cgc ccc cag tca			928
Ala Glu His Met Lys Arg Gln Arg His Pro Arg Leu Arg Pro Gln Ser			
265	270	275	280
gcc cag tct tct ttc cct ccc tcc cct ggt cct tct cct gat gtg caa			976

90/233

Ala Gln Ser Ser Phe Pro Pro Ser Pro Gly Pro Ser Pro Asp Val Gln	
285 290 295	
ctg gca act ctg gct cag aga gtc aag gaa gtt ttg ccc cat gtg cca	1024
Leu Ala Thr Leu Ala Gln Arg Val Lys Glu Val Leu Pro His Val Pro	
300 305 310	
ttg ggt gtc atc cag aga gac ctg gcc aag act ggc tgt gta gac ttg	1072
Leu Gly Val Ile Gln Arg Asp Leu Ala Lys Thr Gly Cys Val Asp Leu	
315 320 325	
act atc act aat ctg ctt gag ggg gcc gta gct ttc atg cct gaa gac	1120
Thr Ile Thr Asn Leu Leu Glu Gly Ala Val Ala Phe Met Pro Glu Asp	
330 335 340	
atc acc aag gga act cag tcc cta ccc aca gcc tct gcc tcc aag ttt	1168
Ile Thr Lys Gly Thr Gln Ser Leu Pro Thr Ala Ser Ala Ser Lys Phe	
345 350 355 360	
ccc agc tct ggc ccg gtg acc cct cag cca aca gcc cta aca ttt gcc	1216
Pro Ser Ser Gly Pro Val Thr Pro Gln Pro Thr Ala Leu Thr Phe Ala	
365 370 375	
aag tct tcc tgg gcc cgg cag gag agc ctg cag gag cgc aag caa gca	1264
Lys Ser Ser Trp Ala Arg Gln Glu Ser Leu Gln Glu Arg Lys Gln Ala	
380 385 390	
cta tat gaa tac gca aga agg aga ttc aca gag aga cga gcc cag gag	1312
Leu Tyr Glu Tyr Ala Arg Arg Arg Phe Thr Glu Arg Arg Ala Gln Glu	
395 400 405	
gct gac tgagctcaaa ggaacaggat ggcacccaga gccgcaggac ggagactggg gg	1370
Ala Asp	
410	
cagccctcac ccaactcaca acaggctgga tgggtgggtg gtaaaaaggg aaggatgagg	1430
ctcccccaat gtcacattaa attcatggtt ttcattcaag gc	1472

<210> 54

<211> 1652

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

91/233

<222> (17)...(1468)

<400> 54

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      Met Glu Glu Gly Gly Gly Gly Val Arg Ser Leu Val
              1              5              10

ccg ggc ggg ccg gtg tta ctg gtc ctc tgc ggc ctc ctg gag gcg tcc      100
Pro Gly Gly Pro Val Leu Leu Val Leu Cys Gly Leu Leu Glu Ala Ser
              15              20              25

ggc ggc ggc cga gcc ctt cct caa ctc agc gat gac atc cct ttc cga      148
Gly Gly Gly Arg Ala Leu Pro Gln Leu Ser Asp Asp Ile Pro Phe Arg
              30              35              40

gtc aac tgg ccc ggc acc gag ttc tct ctg ccc aca act gga gtt tta      196
Val Asn Trp Pro Gly Thr Glu Phe Ser Leu Pro Thr Thr Gly Val Leu
              45              50              55              60

tat aaa gaa gat aat tat gtc atc atg aca act gca cat aaa gaa aaa      244
Tyr Lys Glu Asp Asn Tyr Val Ile Met Thr Thr Ala His Lys Glu Lys
              65              70              75

tat aaa tgc ata ctt ccc ctt gtg aca agt ggg gat gag gaa gaa gaa      292
Tyr Lys Cys Ile Leu Pro Leu Val Thr Ser Gly Asp Glu Glu Glu Glu
              80              85              90

aag gat tat aaa ggc cct aat cca aga gag ctt ttg gag cca cta ttt      340
Lys Asp Tyr Lys Gly Pro Asn Pro Arg Glu Leu Leu Glu Pro Leu Phe
              95              100              105

aaa caa agc agt tgt tcc tac aga att gag tct tat tgg act tac gaa      388
Lys Gln Ser Ser Cys Ser Tyr Arg Ile Glu Ser Tyr Trp Thr Tyr Glu
              110              115              120

gta tgt cat gga aaa cac att cgg cag tac cat gaa gag aaa gaa act      436
Val Cys His Gly Lys His Ile Arg Gln Tyr His Glu Glu Lys Glu Thr
              125              130              135              140

ggc cag aaa ata aat att cac gag tac tac ctt ggg aat atg ttg gcc      484
Gly Gln Lys Ile Asn Ile His Glu Tyr Tyr Leu Gly Asn Met Leu Ala
              145              150              155

aag aac ctt cta ttt gaa aaa gaa cga gaa gca gaa gaa aag gaa aaa      532
Lys Asn Leu Leu Phe Glu Lys Glu Arg Glu Ala Glu Glu Lys Glu Lys
              160              165              170

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tca aat gag att ccc act aaa aat atc gaa ggt cag atg aca cca tac	580
Ser Asn Glu Ile Pro Thr Lys Asn Ile Glu Gly Gln Met Thr Pro Tyr	
175 180 185	
tat cct gtg gga atg gga aat ggt aca cct tgt agt ttg aaa cag aac	628
Tyr Pro Val Gly Met Gly Asn Gly Thr Pro Cys Ser Leu Lys Gln Asn	
190 195 200	
cgg ccc aga tca agt act gtg atg tac ata tgt cat cct gaa tct aag	676
Arg Pro Arg Ser Ser Thr Val Met Tyr Ile Cys His Pro Glu Ser Lys	
205 210 215 220	
cat gaa att ctt tca gta gct gaa gtt aca act tgt gaa tat gaa gtt	724
His Glu Ile Leu Ser Val Ala Glu Val Thr Thr Cys Glu Tyr Glu Val	
225 230 235	
gtc att ttg aca cca ctc ttg tgc agt cat cct aaa tat agg ttc aga	772
Val Ile Leu Thr Pro Leu Leu Cys Ser His Pro Lys Tyr Arg Phe Arg	
240 245 250	
gca tct cct gtg aat gac ata ttt tgt caa tca ctg cca gga tct cca	820
Ala Ser Pro Val Asn Asp Ile Phe Cys Gln Ser Leu Pro Gly Ser Pro	
255 260 265	
ttt aag ccc ctc acc ctg agg cag ctg gag cag cag gaa gaa ata cta	868
Phe Lys Pro Leu Thr Leu Arg Gln Leu Glu Gln Gln Glu Glu Ile Leu	
270 275 280	
agg gtg cct ttt agg aga aat aaa gag gaa gat ttg caa tca act aaa	916
Arg Val Pro Phe Arg Arg Asn Lys Glu Glu Asp Leu Gln Ser Thr Lys	
285 290 295 300	
gaa gag aga ttt cca gcg atc cac aag tcg att gct att ggc tct cag	964
Glu Glu Arg Phe Pro Ala Ile His Lys Ser Ile Ala Ile Gly Ser Gln	
305 310 315	
cca gtg ctc act gtt ggg aca acc cac ata tcc aaa ttg aca gat gac	1012
Pro Val Leu Thr Val Gly Thr Thr His Ile Ser Lys Leu Thr Asp Asp	
320 325 330	
caa ctc ata aaa gag ttt ctt agt ggt tct tac tgc ttt cgt ggg ggt	1060
Gln Leu Ile Lys Glu Phe Leu Ser Gly Ser Tyr Cys Phe Arg Gly Gly	
335 340 345	
gtc ggt tgg tgg aaa tat gaa ttc tgc tat ggc aaa cat gta cat caa	1108
Val Gly Trp Trp Lys Tyr Glu Phe Cys Tyr Gly Lys His Val His Gln	

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350	355	360	
tac cat gag gac aag gat agt ggg aaa acc tct gtg gtt gtc ggg aca			1156
Tyr His Glu Asp Lys Asp Ser Gly Lys Thr Ser Val Val Val Gly Thr			
365	370	375	380
tgg aac caa gaa gag cat att gaa tgg gct aag aag aat act gct aga			1204
Trp Asn Gln Glu Glu His Ile Glu Trp Ala Lys Lys Asn Thr Ala Arg			
385	390	395	
gct tat cat ctt caa gac gat ggt acc cag aca gtc agg atg gtg tca			1252
Ala Tyr His Leu Gln Asp Asp Gly Thr Gln Thr Val Arg Met Val Ser			
400	405	410	
cat ttt tat gga aat gga gat att tgt gat ata act gac aaa cca aga			1300
His Phe Tyr Gly Asn Gly Asp Ile Cys Asp Ile Thr Asp Lys Pro Arg			
415	420	425	
cag gtg act gta aaa cta aag tgc aaa gaa tca gat tca cct cat gct			1348
Gln Val Thr Val Lys Leu Lys Cys Lys Glu Ser Asp Ser Pro His Ala			
430	435	440	
gtt act gta tat atg cta gag cct cac tcc tgt caa tat att ctt ggg			1396
Val Thr Val Tyr Met Leu Glu Pro His Ser Cys Gln Tyr Ile Leu Gly			
445	450	455	460
gtt gaa tct cca gtg atc tgt aaa atc tta gat aca gca gat gaa aat			1444
Val Glu Ser Pro Val Ile Cys Lys Ile Leu Asp Thr Ala Asp Glu Asn			
465	470	475	
gga ctt ctt tct ctc ccc aac taaaggatat taaagttagg ggaaa			1490
Gly Leu Leu Ser Leu Pro Asn			
480			
gaaaagatca ttgaaagtca tgataatttc tgtcccactg tgtctcatta tagagttctc			1550
agccattgga cctcttctaa aggatggtat aaaatgactc tcaaccactt tgtgaataca			1610
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<211> 2112

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<213> Homo sapiens

<220>

<221> CDS

94/233

<222> (20)...(1843)

<400> 55

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              1              5              10

ggc ttt ggg ccc ttc caa ctg cgg aat gtg gca ctg ctg gcc ctg ccc      100
Gly Phe Gly Pro Phe Gln Leu Arg Asn Val Ala Leu Leu Ala Leu Pro
              15              20              25

cga gtg ctg cta cca ctg cac ttc ctc ctg ccc atc ttc ctg gct gcc      148
Arg Val Leu Leu Pro Leu His Phe Leu Leu Pro Ile Phe Leu Ala Ala
              30              35              40

gtg cct gcc cac cga tgt gcc ctg ccg ggt gcc cct gcc aac ttc agc      196
Val Pro Ala His Arg Cys Ala Leu Pro Gly Ala Pro Ala Asn Phe Ser
              45              50              55

cat cag gat gtg tgg ctg gag gcc cat ctt ccc cgg gag cct gat ggc      244
His Gln Asp Val Trp Leu Glu Ala His Leu Pro Arg Glu Pro Asp Gly
              60              65              70              75

acg ctc agc tcc tgc ctc cgc ttt gcc tat ccc cag gct ctc ccc aac      292
Thr Leu Ser Ser Cys Leu Arg Phe Ala Tyr Pro Gln Ala Leu Pro Asn
              80              85              90

acc acg ttg ggg gaa gaa agg cag agc cgt ggg gag ctg gag gat gaa      340
Thr Thr Leu Gly Glu Glu Arg Gln Ser Arg Gly Glu Leu Glu Asp Glu
              95              100              105

cct gcc aca gtg ccc tgc tct cag ggc tgg gag tac gac cac tca gaa      388
Pro Ala Thr Val Pro Cys Ser Gln Gly Trp Glu Tyr Asp His Ser Glu
              110              115              120

ttc tcc tct acc att gca act gag tcc cag gtc ggt att tac ata atc      436
Phe Ser Ser Thr Ile Ala Thr Glu Ser Gln Val Gly Ile Tyr Ile Ile
              125              130              135

cat ctg gag gtg gaa tgt cgg tgg agg cag tct ccc tgg gag gca gca      484
His Leu Glu Val Glu Cys Arg Trp Arg Gln Ser Pro Trp Glu Ala Ala
              140              145              150              155

ggt cga ggc ctt cct tgg gaa gaa gct gag gct gca gga ctg ggg agg      532
Gly Arg Gly Leu Pro Trp Glu Glu Ala Glu Ala Ala Gly Leu Gly Arg
              160              165              170

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95/233

gac aaa gtt tcc tat tcc cca agc tgg cgt gaa tcg ttg gga ggt tta	580
Asp Lys Val Ser Tyr Ser Pro Ser Trp Arg Glu Ser Leu Gly Gly Leu	
175 180 185	
tta tct ggc atg gag tgg gat ctg gtg tgt gag cag aaa ggt ctg aac	628
Leu Ser Gly Met Glu Trp Asp Leu Val Cys Glu Gln Lys Gly Leu Asn	
190 195 200	
aga gct ggc tcc act ttc ttc ttc gcc ggt gtg ctg gtg ggg gct gtg	676
Arg Ala Ala Ser Thr Phe Phe Phe Ala Gly Val Leu Val Gly Ala Val	
205 210 215	
gcc ttt gga tat ctg tcc gac agg ttt ggg cgg cgg cgt ctg ctg ctg	724
Ala Phe Gly Tyr Leu Ser Asp Arg Phe Gly Arg Arg Arg Leu Leu Leu	
220 225 230 235	
gta gcc tac gtg agt acc ctg gtg ctg ggc ctg gca tct gca gcc tcc	772
Val Ala Tyr Val Ser Thr Leu Val Leu Gly Leu Ala Ser Ala Ala Ser	
240 245 250	
gtc agc tat gta atg ttt gcc atc acc cgc acc ctt act ggc tca gcc	820
Val Ser Tyr Val Met Phe Ala Ile Thr Arg Thr Leu Thr Gly Ser Ala	
255 260 265	
ctg gct ggt ttt acc atc atc gtg atg cca ctg gag ctg gag tgg ctg	868
Leu Ala Gly Phe Thr Ile Ile Val Met Pro Leu Glu Leu Glu Trp Leu	
270 275 280	
gat gtg gag cac cgc acc gtg gct gga gtc ctg agc agc acc ttc tgg	916
Asp Val Glu His Arg Thr Val Ala Gly Val Leu Ser Ser Thr Phe Trp	
285 290 295	
aca ggg ggc gtg atg ctg ctg gca ctg gtt ggg tac ctg ata cgg gac	964
Thr Gly Gly Val Met Leu Leu Ala Leu Val Gly Tyr Leu Ile Arg Asp	
300 305 310 315	
tgg cga tgg ctt ctg cta gct gtc acc ctg cct tgt gcc cca ggc atc	1012
Trp Arg Trp Leu Leu Leu Ala Val Thr Leu Pro Cys Ala Pro Gly Ile	
320 325 330	
ctc agc ctc tgg tgg gtg cct gag tct gca cgc tgg ctt ctg acc caa	1060
Leu Ser Leu Trp Trp Val Pro Glu Ser Ala Arg Trp Leu Leu Thr Gln	
335 340 345	
ggc cat gtg aaa gag gcc cac agg tac ttg ctc cac tgt gcc agg ctc	1108
Gly His Val Lys Glu Ala His Arg Tyr Leu Leu His Cys Ala Arg Leu	

96/233

350	355	360	
aat ggg cgg cca gtg tgt gag gac agc ttc agc cag gag gct gtg agc			1156
Asn Gly Arg Pro Val Cys Glu Asp Ser Phe Ser Gln Glu Ala Val Ser			
365	370	375	
aaa gtg gcc gcc ggg gaa cgg gtg gtc cga aga cct tca tac cta gac			1204
Lys Val Ala Ala Gly Glu Arg Val Val Arg Arg Pro Ser Tyr Leu Asp			
380	385	390	395
ctg ttc cgc aca cca cgg ctc cga cac atc tca ctg tgc tgc gtg gtg			1252
Leu Phe Arg Thr Pro Arg Leu Arg His Ile Ser Leu Cys Cys Val Val			
400	405	410	
gtg tgg ttc gga gtg aac ttc tcc tat tac ggc ctg agt ctg gat gtg			1300
Val Trp Phe Gly Val Asn Phe Ser Tyr Tyr Gly Leu Ser Leu Asp Val			
415	420	425	
tcg ggg ctg ggg ctg aac gtg tac cag aca cag ctg ttg ttc ggg gct			1348
Ser Gly Leu Gly Leu Asn Val Tyr Gln Thr Gln Leu Leu Phe Gly Ala			
430	435	440	
gtg gaa ctg ccc tcc aag ctg ctg gtc tac ttg tcg gtg cgc tac gca			1396
Val Glu Leu Pro Ser Lys Leu Leu Val Tyr Leu Ser Val Arg Tyr Ala			
445	450	455	
gga cgc cgc ctc acg caa gcc ggg aca ctg ctg ggc acg gcc ctg gcg			1444
Gly Arg Arg Leu Thr Gln Ala Gly Thr Leu Leu Gly Thr Ala Leu Ala			
460	465	470	475
ttc ggc act aga ctg cta gtg tcc tct gat atg aag tcc tgg agc act			1492
Phe Gly Thr Arg Leu Leu Val Ser Ser Asp Met Lys Ser Trp Ser Thr			
480	485	490	
gtc ctg gca gtg atg ggg aaa gct ttt tct gaa gct gcc ttc acc act			1540
Val Leu Ala Val Met Gly Lys Ala Phe Ser Glu Ala Ala Phe Thr Thr			
495	500	505	
gcc tac ctg ttc act tca gag ttg tac cct acg gtg ctc aga cag aca			1588
Ala Tyr Leu Phe Thr Ser Glu Leu Tyr Pro Thr Val Leu Arg Gln Thr			
510	515	520	
ggg atg ggg ctg act gca ctg gtg ggc cgg ctg ggg ggc tct ttg gcc			1636
Gly Met Gly Leu Thr Ala Leu Val Gly Arg Leu Gly Gly Ser Leu Ala			
525	530	535	
cca ctg gcg gcc ttg ctg gat gga gtg tgg ctg tca ctg ccc aag ctt			1684

97/233

Pro Leu Ala Ala Leu Leu Asp Gly Val Trp Leu Ser Leu Pro Lys Leu
 540 545 550 555
 act tat ggg ggg atc gcc ctg ctg gct gcc ggc acc gcc ctc ctg ctg 1732
 Thr Tyr Gly Gly Ile Ala Leu Leu Ala Ala Gly Thr Ala Leu Leu Leu
 560 565 570
 cca gag acg agg cag gca cag ctg cca gag acc atc cag gac gtg gag 1780
 Pro Glu Thr Arg Gln Ala Gln Leu Pro Glu Thr Ile Gln Asp Val Glu
 575 580 585
 aga aag agt gcc cca acc agt ctt cag gag gaa gag atg ccc atg aag 1828
 Arg Lys Ser Ala Pro Thr Ser Leu Gln Glu Glu Glu Met Pro Met Lys
 590 595 600
 cag gtc cag aac taagtgggag tggaggcagg ccctccacag aagctctgca 1880
 Gln Val Gln Asn
 605
 gcaggggctg ggagagcaga agggcaggcc ctgcaactca ggctgggagt atcgaaccct 1940
 ctgcctaggg ccggagttgc tgccagtacc cgtccctct getcatccat ccttgattat 2000
 ttggcttcta ggaacagttg acttcccaga atgcagtggg ctgctgggca ccctctcac 2060
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 <213> Homo sapiens
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 <222> (33)...(977)
 <400> 56

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 Met Gly Ala Arg Gly Ala Leu
 1 5
 ctg ctg gcg ctg ctg ctg gct cgg gct gga ctc agg aag ccg gag tcg 101
 Leu Leu Ala Leu Leu Leu Ala Arg Ala Gly Leu Arg Lys Pro Glu Ser
 10 15 20
 cag gag gcg gcg ccg tta tca gga cca tgc ggc cga cgg gtc atc acg 149
 Gln Glu Ala Ala Pro Leu Ser Gly Pro Cys Gly Arg Arg Val Ile Thr

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25	30	35	
tcg cgc atc gtg ggt gga gag gac gcc gaa ctc ggg cgt tgg ccg tgg			197
Ser Arg Ile Val Gly Gly Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp			
40	45	50	55
cag ggg agc ctg cgc ctg tgg gat tcc cac gta tgc gga gtg agc ctg			245
Gln Gly Ser Leu Arg Leu Trp Asp Ser His Val Cys Gly Val Ser Leu			
60	65	70	
ctc agc cac cgc tgg gca ctc acg gcg gcg cac tgc ttt gaa acc tat			293
Leu Ser His Arg Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr			
75	80	85	
agt gac ctt agt gat ccc tcc ggg tgg atg gtc cag ttt ggc cag ctg			341
Ser Asp Leu Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu			
90	95	100	
act tcc atg cca tcc ttc tgg agc ctg cag gcc tac tac acc cgt tac			389
Thr Ser Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr			
105	110	115	
ttc gta tcg aat atc tat ctg agc cct cgc tac ctg ggg aat tca ccc			437
Phe Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro			
120	125	130	135
tat gac att gcc ttg gtg aag ctg tct gca cct gtc acc tac act aaa			485
Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr Lys			
140	145	150	
cac atc cag ccc atc tgt ctc cag gcc tcc aca ttt gag ttt gag aac			533
His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe Glu Asn			
155	160	165	
cgg aca gac tgc tgg gtg act ggc tgg ggg tac atc aaa gag gat gag			581
Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys Glu Asp Glu			
170	175	180	
gca ctg cca tct ccc cac acc ctc cag gaa gtt cag gtc gcc atc ata			629
Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln Val Ala Ile Ile			
185	190	195	
aac aac tct atg tgc aac cac ctc ttc ctc aag tac agt ttc cgc aag			677
Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys Tyr Ser Phe Arg Lys			
200	205	210	215
gac atc ttt gga gac atg gtt tgt gct ggc aat gcc caa ggc ggg aag			725

99/233

Asp Ile Phe Gly Asp Met Val Cys Ala Gly Asn Ala Gln Gly Gly Lys
 220 225 230
 gat gcc tgc ttc ggt gac tca ggt gga ccc ttg gcc tgt aac aag aat 773
 Asp Ala Cys Phe Gly Asp Ser Gly Gly Pro Leu Ala Cys Asn Lys Asn
 235 240 245
 gga ctg tgg tat cag att gga gtc gtg agc tgg gga gtg ggc tgt ggt 821
 Gly Leu Trp Tyr Gln Ile Gly Val Val Ser Trp Gly Val Gly Cys Gly
 250 255 260
 cgg ccc aat cgg ccc ggt gtc tac acc aat atc agc cac cac ttt gag 869
 Arg Pro Asn Arg Pro Gly Val Tyr Thr Asn Ile Ser His His Phe Glu
 265 270 275
 tgg atc cag aag ctg atg gcc cag agt ggc atg tcc cag cca gac ccc 917
 Trp Ile Gln Lys Leu Met Ala Gln Ser Gly Met Ser Gln Pro Asp Pro
 280 285 290 295
 tcc tgg ccg cta ctc ttt ttc cct ctt ctc tgg gct ctc cca ctc ctg 965
 Ser Trp Pro Leu Leu Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu
 300 305 310
 ggg ccg gtc tgagcctacc tgagcccatg cagcctgggg ccaactgccaa gtcagg 1020
 Gly Pro Val

ccctgggttct cttctgtctt gtttggtaat aaacacattc cagttgatgc cttgcagggc 1080
 attcttc 1087

<210> 57

<211> 1694

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (216)...(500)

<400> 57

ccgaagttt gaggggtgtg gacggtttgt gacccctta gccgacccta ctcctcactg 60
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 cccatggacc ccagtccaac gccgaggga taggaccatc caaaagcgga accttcgcct 180
 cagaaaaagg cgtggacct gccagcagcc aggcc atg gag ctc tet gat gtc 233

100/233

		Met	Glu	Leu	Ser	Asp	Val									
		1					5									
acc	ctc	att	gag	ggt	gtg	ggt	aat	gag	gtg	atg	gtg	gtg	gca	ggt	gtg	281
Thr	Leu	Ile	Glu	Gly	Val	Gly	Asn	Glu	Val	Met	Val	Val	Ala	Gly	Val	
		10			15			20								
gtg	gtg	ctg	att	cta	gcc	ttg	gtc	cta	gct	tgg	ctc	tct	acc	tac	gta	329
Val	Val	Leu	Ile	Leu	Ala	Leu	Val	Leu	Ala	Trp	Leu	Ser	Thr	Tyr	Val	
		25			30			35								
gca	gac	agc	ggt	agc	aac	cag	ctc	ctg	ggc	gct	att	gtg	tca	gca	ggc	377
Ala	Asp	Ser	Gly	Ser	Asn	Gln	Leu	Leu	Gly	Ala	Ile	Val	Ser	Ala	Gly	
		40			45			50								
gac	aca	tcc	gtc	ctc	cac	ctg	ggg	cat	gtg	gac	cac	ctg	gtg	gca	ggc	425
Asp	Thr	Ser	Val	Leu	His	Leu	Gly	His	Val	Asp	His	Leu	Val	Ala	Gly	
		55			60			65			70					
caa	ggc	aac	ccc	gag	cca	act	gaa	ctc	ccc	cat	cca	tca	gag	gca	aat	473
Gln	Gly	Asn	Pro	Glu	Pro	Thr	Glu	Leu	Pro	His	Pro	Ser	Glu	Ala	Asn	
		75			80			85								
act	tcc	ctg	gac	aag	aaa	gcc	aga	tgaaactgat	ctaccagggc	cgc						520
Thr	Ser	Leu	Asp	Lys	Lys	Ala	Arg									
		90														
ctgctacaag	acccagcccg	cacactgcgt	tctctgaaca	ttaccgacaa	ctgtgtgatt											580
cactgccacc	gtccaccccc	agggtcagct	gttccaggcc	cctcagcctc	cttggecccc											640
tgggccactg	agccacccag	ccttggtgtc	aatgtgggca	gcctcatggt	gcctgtcttt											700
gtggtgctgt	tgggtgtggt	ctggtaacttc	cgaatcaatt	accgccaatt	cttcacagca											760
cctgccactg	tctccctggt	gggagtcacc	gtcttcttca	gcttcctagt	atttgggatg											820
tatggacgat	aaggacatag	gaagaaaatg	aaaggcatgg	tctttctcct	tatatggcctc											880
cccacttttc	ctggccagag	ctgggcccaa	gggccgggga	gggaggggtg	gaaaggatgt											940
gatggaaato	tcctocatag	gacacaggag	gcaagtatgc	ggcctccctt	tctcatccac											1000
aggagtacag	atgtccctcc	cgtgcgagca	caactcaggt	agaaatgagg	atgtcatctt											1060
ccttcacttt	tagggtcctc	tgaaggagtt	caaagctgct	ggccaagctc	agtggggagc											1120
ctgggctctg	agattccctc	ccacctgtgg	ttctgactct	tcccagtgtc	ctgcatgtct											1180
gccccagca	cccagggtcg	cctgcaaggg	cagctcagca	tggccccagc	acaactccgt											1240
agggagcctg	gagtatcctt	ccattttctc	gccccatact	catcttttga	gactgaaatc											1300
acactggcgg	gaatgaagat	tgtgccagcc	ttctcttatg	ggcacctagc	cgccttcacc											1360
ttcttctctt	accccttagc	aggaataggg	tgtcctccct	tctttcaaag	cactttgctt											1420

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gcattttatt ttattttttt aagagtcctt catagagctc agtcaggaag gggatggggc 1480
 accaagccaa gccccagca ttgggagcgg ccaggccaca gctgctgctc ccgtagtcct 1540
 caggctgtaa gcaagagaca gcaactggccc ttggccagcg tcctaccctg cccaactcca 1600
 aggactgggt atggattgct gggccctagg ctcttgcttc tggggctatt ggagggtcag 1660
 tgtctgtgac tgaataaagt tccattttgt ggtc 1694

<210> 58

<211> 1522

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (12)...(668)

<400> 58

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 Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln
 1 5 10
 ctg atc atg cag ttg ggt tcg gtg ctg ctc aca cgc tgc ccc ttt tgg 98
 Leu Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp
 15 20 25
 ggc tgc ttc agc cag ctc atg ctg tac gct gag agg gct gag gca cgc 146
 Gly Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg
 30 35 40 45
 cgg aag ccc gac atc cca gtg cct tac ctg tat ttc gac atg ggg gca 194
 Arg Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala
 50 55 60
 gcc gtg ctg tgc gct agt ttc atg tcc ttt ggc gtg aag cgg cgc tgg 242
 Ala Val Leu Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp
 65 70 75
 ttc gcg ctg ggg gcc gca ctc caa ttg gcc att agc acc tac gcc gcc 290
 Phe Ala Leu Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala
 80 85 90
 tac atc ggg ggc tac gtc cac tac ggg gac tgg ctg aag gtc cgt atg 338
 Tyr Ile Gly Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met
 95 100 105

102/233

tac tcg cgc aca gtt gcc atc atc ggc gga ctt tct tgt gtt ggc cag	386
Tyr Ser Arg Thr Val Ala Ile Ile Gly Gly Leu Ser Cys Val Gly Gln	
110 115 120 125	
cgg tgc tgg gga gct gta ccg ccg gaa acc tcg cag ccg ctc cct gca	434
Arg Cys Trp Gly Ala Val Pro Pro Glu Thr Ser Gln Pro Leu Pro Ala	
130 135 140	
gtc cac cgg cca ggt gtt cct ggg tat cta cct cat ctg tgt ggc cta	482
Val His Arg Pro Gly Val Pro Gly Tyr Leu Pro His Leu Cys Gly Leu	
145 150 155	
ctc act gca gca cag caa gga gga ccg gct ggc gta tct gaa cca tct	530
Leu Thr Ala Ala Gln Gln Gly Gly Pro Ala Gly Val Ser Glu Pro Ser	
160 165 170	
ccc agg agg gga gct gat gat cca gct gtt ctt cgt gct gta tgg cat	578
Pro Arg Arg Gly Ala Asp Asp Pro Ala Val Leu Arg Ala Val Trp His	
175 180 185	
cct ggc cct ggc ctt tct gtc agg cta cta cgt gac cct cgc tgc cca	626
Pro Gly Pro Gly Leu Ser Val Arg Leu Leu Arg Asp Pro Arg Cys Pro	
190 195 200 205	
gat cct ggc tgt act gct gcc ccc tgt cat gct gct cat tgatg	670
Asp Pro Gly Cys Thr Ala Ala Pro Cys His Ala Ala His	
210 215	
gcaatgttgc ttactggcac aacacgcggc gtgttgagtt ctggaaccag atgaagctcc	730
ttggagagag tgtgggcata ttccgaactg ctgtcatctg gccactgatg gotgagtttt	790
atggcaagag gotgagatgg gcacagggag ccactgaggg tcacctgcc ttctctcttg	850
ctggcccagc tgetgtttat ttatgctttt tggctctgtt gtttgatctt ttgtttttt	910
aaaattgttt ttgacagtta agaggcagct catttgtcca aatttctggg ctcagcgctt	970
gggagggcag gagccctggc actaatgctg tacaggtttt tttctgttta ggagagctga	1030
ggccagctgc ccactgagtc tctgtccct gagaaggagg tatggcaggg ctgggatgcg	1090
gctactgaga gtgggagagt gggagacaga ggaaggaaga tggagattgg aagtgagcaa	1150
atgtgaaaaa ttctcttttg aacctggcag atgcagctag gctctgcagt gctgttttga	1210
gactgtgaga gggagtgcgt gtgttgacac atgtggatca ggccaggaa gggcacaggg	1270
gctgagcact acagaagtca catgggttct cagggatgc caggggcaga aacagtaccg	1330
gctctctgtc actcaccttg agagtagagc agaccctgtt ctgctctggg ctgtgaaggg	1390
gtggagcagg cagtggccag ctttggccct cctgctgtct ctgtttctag ctccatggtt	1450
ggcctggtgg ggggtggagt cctcccaaa caccagacca cacagtctc caaaaataaa	1510

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cattttatat ag

1522

<210> 59

<211> 1591

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (44)...(1426)

<400> 59

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Met Phe Thr Ile

1

aag ctc ctt ctt ttt att gtt cct cta gtt att tcc tcc aga att gat 103

Lys Leu Leu Leu Phe Ile Val Pro Leu Val Ile Ser Ser Arg Ile Asp

5

10

15

20

caa gac aat tca tca ttt gat tct cta tct cca gag cca aaa tca aga 151

Gln Asp Asn Ser Ser Phe Asp Ser Leu Ser Pro Glu Pro Lys Ser Arg

25

30

35

ttt gct atg tta gac gat gta aaa att tta gcc aat ggc ctc ctt cag 199

Phe Ala Met Leu Asp Asp Val Lys Ile Leu Ala Asn Gly Leu Leu Gln

40

45

50

ttg gga cat ggt ctt aaa gac ttt gtc cat aag acg aag ggc caa att 247

Leu Gly His Gly Leu Lys Asp Phe Val His Lys Thr Lys Gly Gln Ile

55

60

65

aat gac ata ttt caa aaa ctc aac ata ttt gat cag tct ttt tat gat 295

Asn Asp Ile Phe Gln Lys Leu Asn Ile Phe Asp Gln Ser Phe Tyr Asp

70

75

80

cta tcg ctg caa acc agt gaa atc aaa gaa gaa gaa aag gaa ctg aga 343

Leu Ser Leu Gln Thr Ser Glu Ile Lys Glu Glu Glu Lys Glu Leu Arg

85

90

95

100

aga act aca tat aaa cta caa gtc aaa aat gaa gag gta aag aat atg 391

Arg Thr Thr Tyr Lys Leu Gln Val Lys Asn Glu Glu Val Lys Asn Met

105

110

115

tca ctt gaa ctc aac tca aaa ctt gaa agc ctc cta gaa gaa aaa att 439

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Ser Leu Glu Leu Asn Ser Lys Leu Glu Ser Leu Leu Glu Glu Lys Ile
 120 125 130
 cta ctt caa caa aaa gtg aaa tat tta gaa gag caa cta act aac tta 487
 Leu Leu Gln Gln Lys Val Lys Tyr Leu Glu Glu Gln Leu Thr Asn Leu
 135 140 145
 att caa aat caa cct gaa act cca gaa cac cca gaa gta act tca ctt 535
 Ile Gln Asn Gln Pro Glu Thr Pro Glu His Pro Glu Val Thr Ser Leu
 150 155 160
 aaa act ttt gta gaa aaa caa gat aat agc atc aaa gac ctt ctc cag 583
 Lys Thr Phe Val Glu Lys Gln Asp Asn Ser Ile Lys Asp Leu Leu Gln
 165 170 175 180
 acc gtg gaa gac caa tat aaa caa tta aac caa cag cat agt caa ata 631
 Thr Val Glu Asp Gln Tyr Lys Gln Leu Asn Gln Gln His Ser Gln Ile
 185 190 195
 aaa gaa ata gaa aat cag ctc aga agg act agt att caa gaa ccc aca 679
 Lys Glu Ile Glu Asn Gln Leu Arg Arg Thr Ser Ile Gln Glu Pro Thr
 200 205 210
 gaa att tct cta tct tcc aag cca aga gca cca aga act act ccc ttt 727
 Glu Ile Ser Leu Ser Ser Lys Pro Arg Ala Pro Arg Thr Thr Pro Phe
 215 220 225
 ctt cag ttg aat gaa ata aga aat gta aaa cat gat ggc att cct gct 775
 Leu Gln Leu Asn Glu Ile Arg Asn Val Lys His Asp Gly Ile Pro Ala
 230 235 240
 gaa tgt acc acc att tat aac aga ggt gaa cat aca agt ggc atg tat 823
 Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu His Thr Ser Gly Met Tyr
 245 250 255 260
 gcc atc aga ccc agc aac tct caa gtt ttt cat gtc tac tgt gat gtt 871
 Ala Ile Arg Pro Ser Asn Ser Gln Val Phe His Val Tyr Cys Asp Val
 265 270 275
 ata tca ggt agt cca tgg aca tta att caa cat cga ata gat gga tca 919
 Ile Ser Gly Ser Pro Trp Thr Leu Ile Gln His Arg Ile Asp Gly Ser
 280 285 290
 caa aac ttc aat gaa acg tgg gag aac tac aaa tat ggt ttt ggg agg 967
 Gln Asn Phe Asn Glu Thr Trp Glu Asn Tyr Lys Tyr Gly Phe Gly Arg
 295 300 305

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ctt gat gga gaa ttt tgg ttg ggc cta gag aag ata tac tcc ata gtg      1015
Leu Asp Gly Glu Phe Trp Leu Gly Leu Glu Lys Ile Tyr Ser Ile Val
      310              315              320
aag caa tct aat tat gtt tta cga att gag ctg gaa gac tgg aaa gac      1063
Lys Gln Ser Asn Tyr Val Leu Arg Ile Glu Leu Glu Asp Trp Lys Asp
      325              330              335              340
aac aaa cat tat att gaa tat tct ttt tac ttg gga aat cac gaa acc      1111
Asn Lys His Tyr Ile Glu Tyr Ser Phe Tyr Leu Gly Asn His Glu Thr
      345              350              355
aac tat acg cta cat cta gtt gcg att act ggc aat gtc ccc aat gca      1159
Asn Tyr Thr Leu His Leu Val Ala Ile Thr Gly Asn Val Pro Asn Ala
      360              365              370
atc ccg gaa aac aaa gat ttg gtg ttt tct act tgg gat cac aaa gca      1207
Ile Pro Glu Asn Lys Asp Leu Val Phe Ser Thr Trp Asp His Lys Ala
      375              380              385
aaa gga cac ttc aac tgt cca gag ggt tat tca gga ggc tgg tgg tgg      1255
Lys Gly His Phe Asn Cys Pro Glu Gly Tyr Ser Gly Gly Trp Trp Trp
      390              395              400
cat gat gag tgt gga gaa aac aac cta aat ggt aaa tat aac aaa cca      1303
His Asp Glu Cys Gly Glu Asn Asn Leu Asn Gly Lys Tyr Asn Lys Pro
      405              410              415              420
aga gca aaa tct aag cca gag agg aga aga gga tta tct tgg aag tct      1351
Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg Gly Leu Ser Trp Lys Ser
      425              430              435
caa aat gga agg tta tac tct ata aaa tca acc aaa atg ttg atc cat      1399
Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser Thr Lys Met Leu Ile His
      440              445              450
cca aca gat tca gaa agc ttt gaa tgaactgagg caaatttaaa aggcaat      1450
Pro Thr Asp Ser Glu Ser Phe Glu
      455              460
aatTTaaaca ttaacotcat tccaagttaa tgtggtotaa taatctggta ttaaatectt      1510
aagagaaagc ttgagaaata gatttttttt tatcttaaag tcaactgtcta ttaagatta      1570
aacatacaat cacataacct t                                          1591

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<210> 60

106/233

<211> 1249

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (134)...(784)

<400> 60

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aacagtctgt ggagacagtt gtgtccctgt ggctttggtg cgcctgtgtg cactttctcc      60
ctccacctgg agcatgggct aacaccggag gaaaggaaaa gacagagtca gacagggagc      120
ctggggagggg gcc atg gtg cca atg cac tta ctg ggg aga ctg gag aag      169
      Met Val Pro Met His Leu Leu Gly Arg Leu Glu Lys
              1              5              10
ccg ctt ctc ctc ctg tgc tgc gcc tcc ttc cta ctg ggg ctg gct ttg      217
Pro Leu Leu Leu Leu Cys Cys Ala Ser Phe Leu Leu Gly Leu Ala Leu
              15              20              25
ctg ggc ata aag acg gac atc acc ccc gtt gct tat ttc ttt ctc aca      265
Leu Gly Ile Lys Thr Asp Ile Thr Pro Val Ala Tyr Phe Phe Leu Thr
              30              35              40
ttg ggt ggc ttc ttc ttg ttt gcc tat ctc ctg gtc cgg ttt ctg gaa      313
Leu Gly Gly Phe Phe Leu Phe Ala Tyr Leu Leu Val Arg Phe Leu Glu
              45              50              55              60
tgg ggg ctt cgg tcc cag ctc caa tca atg cag act gag agc cca ggg      361
Trp Gly Leu Arg Ser Gln Leu Gln Ser Met Gln Thr Glu Ser Pro Gly
              65              70              75
ccc tca ggc aat gca cgg gac aat gaa gcc ttt gaa gtg cca gtc tat      409
Pro Ser Gly Asn Ala Arg Asp Asn Glu Ala Phe Glu Val Pro Val Tyr
              80              85              90
gaa gag gcc gtg gtg gga cta gaa tcc cag tgc cgc ccc caa gag ttg      457
Glu Glu Ala Val Val Gly Leu Glu Ser Gln Cys Arg Pro Gln Glu Leu
              95              100              105
gac caa cca ccc ccc tac agc act gtt gtg ata ccc cca gca cct gag      505
Asp Gln Pro Pro Pro Tyr Ser Thr Val Val Ile Pro Pro Ala Pro Glu
              110              115              120
gag gaa caa cct agc cat cca gag ggg tcc agg aga gcc aaa ctg gaa      553
Glu Glu Gln Pro Ser His Pro Glu Gly Ser Arg Arg Ala Lys Leu Glu

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125	130	135	140	
cag agg cga atg gcc tca gag ggg tcc atg gcc cag gaa gga agc cct				601
Gln Arg Arg Met Ala Ser Glu Gly Ser Met Ala Gln Glu Gly Ser Pro				
	145	150	155	
gga aga gct cca atc aac ctt cgg ctt cgg gga cca cgg gct gtg tcc				649
Gly Arg Ala Pro Ile Asn Leu Arg Leu Arg Gly Pro Arg Ala Val Ser				
	160	165	170	
act gct cct gat ctg cag agc ttg gcg gca gtc ccc aca tta gag cct				697
Thr Ala Pro Asp Leu Gln Ser Leu Ala Ala Val Pro Thr Leu Glu Pro				
	175	180	185	
ctg act cca ccc cct gcc tat gat gtc tgc ttt ggt cac cct gat gat				745
Leu Thr Pro Pro Pro Ala Tyr Asp Val Cys Phe Gly His Pro Asp Asp				
	190	195	200	
gat agt gtt ttt tat gag gac aac tgg gca ccc cct taaatgact				790
Asp Ser Val Phe Tyr Glu Asp Asn Trp Ala Pro Pro				
205	210	215		
ctcccaagat ttctcttctc tccacaccag acctcgttca ttgactaac attttccagc				850
gcctactatg tgtcagaaac aagtgtttct gcctggacat cataaatggg gacttggacc				910
ctgaggagag tcaggccacg gtaagccctt cccagctgag atatgggtgg cataatttga				970
gtcttcttggc aacatttgggt gacctacccc atatccaata tttccagcgt tagattgagg				1030
atgaggtagg gaggtgatcc agagaaggcg gagaaggaag aagtaacctc tgagtggcgg				1090
ctattgcttc tgttccagggt gctgttcgag ctgttagaac ccttaggctt gacagctttg				1150
tgagttatta ttgaaaaatg aggattccaa gagtcagagg agtttgataa tgtgcacgag				1210
ggcacactgc tagtaaataa cattaaaata actggaatg				1249

<210> 61

<211> 392

<212> PRT

<213> Homo sapiens

<400> 61

Met	Glu	Gly	Val	Ser	Ala	Leu	Leu	Ala	Arg	Cys	Pro	Thr	Ala	Gly	Leu
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Ala	Gly	Gly	Leu	Gly	Val	Thr	Ala	Cys	Ala	Ala	Ala	Gly	Val	Leu	Leu
			20						25					30	
Tyr	Arg	Ile	Ala	Arg	Arg	Met	Lys	Pro	Thr	His	Thr	Met	Val	Asn	Cys

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35	40	45
Trp Phe Cys Asn Gln Asp Thr Leu Val Pro Tyr Gly Asn Arg Asn Cys		
50	55	60
Trp Asp Cys Pro His Cys Glu Gln Tyr Asn Gly Phe Gln Glu Asn Gly		
65	70	75
Asp Tyr Asn Lys Pro Ile Pro Ala Gln Tyr Leu Glu His Leu Asn His		
85	90	95
Val Val Ser Ser Ala Pro Ser Leu Arg Asp Pro Ser Gln Pro Gln Gln		
100	105	110
Trp Val Ser Ser Gln Val Leu Leu Cys Lys Arg Cys Asn His His Gln		
115	120	125
Thr Thr Lys Ile Lys Gln Leu Ala Ala Phe Ala Pro Arg Glu Glu Gly		
130	135	140
Arg Tyr Asp Glu Glu Val Glu Val Tyr Arg His His Leu Glu Gln Met		
145	150	155
Tyr Lys Leu Cys Arg Pro Cys Gln Ala Ala Val Glu Tyr Tyr Ile Lys		
165	170	175
His Gln Asn Arg Gln Leu Arg Ala Leu Leu Leu Ser His Gln Phe Lys		
180	185	190
Arg Arg Glu Ala Asp Gln Thr His Ala Gln Asn Phe Ser Ser Ala Val		
195	200	205
Lys Ser Pro Val Gln Val Ile Leu Leu Arg Ala Leu Ala Phe Leu Ala		
210	215	220
Cys Ala Phe Leu Leu Thr Thr Ala Leu Tyr Gly Ala Ser Gly His Phe		
225	230	235
Ala Pro Gly Thr Thr Val Pro Leu Ala Leu Pro Pro Gly Gly Asn Gly		
245	250	255
Ser Ala Thr Pro Asp Asn Gly Thr Thr Pro Gly Ala Glu Gly Trp Arg		
260	265	270
Gln Leu Leu Gly Leu Leu Pro Glu His Met Ala Glu Lys Leu Cys Glu		
275	280	285
Ala Trp Ala Phe Gly Gln Ser His Gln Thr Gly Val Val Ala Leu Gly		
290	295	300
Leu Leu Thr Cys Leu Leu Ala Met Leu Leu Ala Gly Arg Ile Arg Leu		
305	310	315
		320

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Arg Arg Ile Asp Ala Phe Cys Thr Cys Leu Trp Ala Leu Leu Leu Gly
 325 330 335
 Leu His Leu Ala Glu Gln His Leu Gln Ala Ala Ser Pro Ser Trp Leu
 340 345 350
 Asp Thr Leu Lys Phe Ser Thr Thr Ser Leu Cys Cys Leu Val Gly Phe
 355 360 365
 Thr Ala Ala Val Ala Thr Arg Lys Ala Thr Gly Pro Arg Arg Phe Arg
 370 375 380
 Pro Arg Arg Ser Glu Lys Gln Pro
 385 390

<210> 62

<211> 497

<212> PRT

<213> Homo sapiens

<400> 62

Met Ala Leu Trp Arg Gly Ser Ala Tyr Ala Gly Phe Leu Ala Leu Ala
 1 5 10 15
 Val Gly Cys Val Phe Leu Leu Glu Pro Glu Leu Pro Gly Ser Ala Leu
 20 25 30
 Arg Ser Leu Trp Ser Ser Leu Cys Leu Gly Pro Ala Pro Ala Pro Pro
 35 40 45
 Gly Pro Val Ser Pro Glu Gly Arg Leu Ala Ala Ala Trp Asp Ala Leu
 50 55 60
 Ile Val Arg Pro Val Arg Arg Trp Arg Arg Val Ala Val Gly Val Asn
 65 70 75 80
 Ala Cys Val Asp Val Val Leu Ser Gly Val Lys Leu Leu Gln Ala Leu
 85 90 95
 Gly Leu Ser Pro Gly Asn Gly Lys Asp His Ser Ile Leu His Ser Arg
 100 105 110
 Asn Asp Leu Glu Glu Ala Phe Ile His Phe Met Trp Lys Gly Ala Ala
 115 120 125
 Ala Glu Arg Phe Phe Ser Asp Lys Glu Thr Phe His Asp Ile Ala Gln
 130 135 140
 Val Ala Ser Glu Phe Pro Gly Ala Gln His Tyr Val Gly Gly Asn Ala

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145	150	155	160
Ala Leu Ile Gly Gln Lys Phe Ala Ala Asn Ser Asp Leu Lys Val Leu			
165	170	175	
Leu Cys Gly Pro Val Gly Pro Arg Leu His Glu Leu Leu Asp Asp Asn			
180	185	190	
Val Phe Val Pro Pro Glu Ser Leu Gln Glu Val Asp Glu Phe His Leu			
195	200	205	
Ile Leu Glu Tyr Gln Ala Gly Glu Glu Trp Gly Gln Leu Lys Ala Pro			
210	215	220	
His Ala Asn Arg Phe Ile Phe Ser His Asp Leu Ser Asn Gly Ala Met			
225	230	235	240
Asn Met Leu Glu Val Phe Val Ser Ser Leu Glu Glu Phe Gln Pro Asp			
245	250	255	
Leu Val Val Leu Ser Gly Leu His Met Met Glu Gly Gln Ser Lys Glu			
260	265	270	
Leu Gln Arg Lys Arg Leu Leu Glu Val Val Thr Ser Ile Ser Asp Ile			
275	280	285	
Pro Thr Gly Ile Pro Val His Leu Glu Leu Ala Ser Met Thr Asn Arg			
290	295	300	
Glu Leu Met Ser Ser Ile Val His Gln Gln Val Phe Pro Ala Val Thr			
305	310	315	320
Ser Leu Gly Leu Asn Glu Gln Glu Leu Leu Phe Leu Thr Gln Ser Ala			
325	330	335	
Ser Gly Pro His Ser Ser Leu Ser Ser Trp Asn Gly Val Pro Asp Val			
340	345	350	
Gly Met Val Ser Asp Ile Leu Phe Trp Ile Leu Lys Glu His Gly Arg			
355	360	365	
Ser Lys Ser Arg Ala Ser Asp Leu Thr Arg Ile His Phe His Thr Leu			
370	375	380	
Val Tyr His Ile Leu Ala Thr Val Asp Gly His Trp Ala Asn Gln Leu			
385	390	395	400
Ala Ala Val Ala Ala Gly Ala Arg Val Ala Gly Thr Gln Ala Cys Ala			
405	410	415	
Thr Glu Thr Ile Asp Thr Ser Arg Val Ser Leu Arg Ala Pro Gln Glu			
420	425	430	

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Phe Met Thr Ser His Ser Glu Ala Gly Ser Arg Ile Val Leu Asn Pro
 435 440 445
 Asn Lys Pro Val Val Glu Trp His Arg Glu Gly Ile Ser Phe His Phe
 450 455 460
 Thr Pro Val Leu Val Cys Lys Asp Pro Ile Arg Thr Val Gly Leu Gly
 465 470 475 480
 Asp Ala Ile Ser Ala Glu Gly Leu Phe Tyr Ser Glu Val His Pro His
 485 490 495
 Tyr

<210> 63

<211> 417

<212> PRT

<213> Homo sapiens

<400> 63

Met Leu Val His Leu Phe Arg Val Gly Ile Arg Gly Gly Pro Phe Pro
 1 5 10 15
 Gly Arg Leu Leu Pro Pro Leu Arg Phe Gln Thr Phe Ser Ala Val Arg
 20 25 30
 Tyr Ser Asp Gly Tyr Arg Ser Ser Ser Leu Leu Arg Ala Val Ala His
 35 40 45
 Leu Arg Ser Gln Leu Trp Ala His Leu Pro Arg Ala Pro Leu Ala Pro
 50 55 60
 Arg Trp Ser Pro Ser Ala Trp Cys Trp Val Gly Gly Ala Leu Leu Gly
 65 70 75 80
 Pro Met Val Leu Ser Lys His Pro His Leu Cys Leu Val Ala Leu Cys
 85 90 95
 Glu Ala Glu Glu Ala Pro Pro Ala Ser Ser Thr Pro His Val Val Gly
 100 105 110
 Ser Arg Phe Asn Trp Lys Leu Phe Trp Gln Phe Leu His Pro His Leu
 115 120 125
 Leu Val Leu Gly Val Ala Val Val Leu Ala Leu Gly Ala Ala Leu Val
 130 135 140
 Asn Val Gln Ile Pro Leu Leu Leu Gly Gln Leu Val Glu Val Val Ala
 145 150 155 160

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Lys Tyr Thr Arg Asp His Val Gly Ser Phe Met Thr Glu Ser Gln Asn
 165 170 175
 Leu Ser Thr His Leu Leu Ile Leu Tyr Gly Val Gln Gly Leu Leu Thr
 180 185 190
 Phe Gly Tyr Leu Val Leu Leu Ser His Val Gly Glu Arg Met Ala Val
 195 200 205
 Asp Met Arg Arg Ala Leu Phe Ser Ser Leu Leu Arg Tyr Cys Gln Pro
 210 215 220
 Gln Gly Ala Glu Leu Gly Gln Asp Ile Thr Phe Phe Asp Ala Asn Lys
 225 230 235 240
 Thr Gly Gln Leu Val Ser Arg Leu Thr Thr Asp Val Gln Glu Phe Lys
 245 250 255
 Ser Ser Phe Lys Leu Val Ile Ser Gln Gly Leu Arg Ser Cys Thr Gln
 260 265 270
 Val Ala Gly Cys Leu Val Ser Leu Ser Met Leu Ser Thr Arg Leu Thr
 275 280 285
 Leu Leu Leu Met Val Ala Thr Pro Ala Leu Met Gly Val Gly Thr Leu
 290 295 300
 Met Gly Ser Gly Leu Arg Lys Leu Ser Cys Gln Cys Gln Glu Gln Ile
 305 310 315 320
 Ala Arg Ala Met Gly Val Ala Asp Glu Ala Leu Gly Asn Val Arg Thr
 325 330 335
 Val Arg Ala Phe Ala Met Glu Gln Arg Glu Glu Glu Arg Tyr Gly Ala
 340 345 350
 Glu Leu Glu Ala Cys Arg Cys Arg Ala Glu Glu Leu Gly Arg Gly Ile
 355 360 365
 Ala Leu Phe Gln Gly Leu Ser Asn Ile Ala Phe Asn Cys Met Val Leu
 370 375 380
 Gly Thr Leu Phe Ile Gly Gly Ser Leu Val Ala Gly Gln Gln Leu Thr
 385 390 395 400
 Gly Gly Asp Leu Met Ser Phe Leu Val Ala Ser Gln Thr Val Gln Arg
 405 410 415
 Leu

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<211> 649

<212> PRT

<213> Homo sapiens

<400> 64

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Met Ile Pro Asn Gln His Asn Ala Gly Ala Gly Ser His Gln Pro Ala
  1             5             10             15
Val Phe Arg Met Ala Val Leu Asp Thr Asp Leu Asp His Ile Leu Pro
      20             25             30
Ser Ser Val Leu Pro Pro Phe Trp Ala Lys Leu Val Val Gly Ser Val
      35             40             45
Ala Ile Val Cys Phe Ala Arg Ser Tyr Asp Gly Asp Phe Val Phe Asp
      50             55             60
Asp Ser Glu Ala Ile Val Asn Asn Lys Val Ala Gly Val Val Gly Arg
      65             70             75             80
Ala Asp Leu Leu Cys Ala Leu Phe Phe Leu Leu Ser Phe Leu Gly Tyr
      85             90             95
Cys Lys Ala Phe Arg Glu Ser Asn Lys Glu Gly Ala His Ser Ser Thr
      100            105            110
Phe Trp Val Leu Leu Ser Ile Phe Leu Gly Ala Val Ala Met Leu Cys
      115            120            125
Lys Glu Gln Gly Ile Thr Val Leu Gly Leu Asn Ala Val Phe Asp Ile
      130            135            140
Leu Val Ile Gly Lys Phe Asn Val Leu Glu Ile Val Gln Lys Val Leu
      145            150            155            160
His Lys Asp Lys Ser Leu Glu Asn Leu Gly Met Leu Arg Asn Gly Gly
      165            170            175
Leu Leu Phe Arg Met Thr Leu Leu Thr Ser Gly Gly Ala Gly Met Leu
      180            185            190
Tyr Val Arg Trp Arg Ile Met Gly Thr Gly Pro Pro Ala Phe Thr Glu
      195            200            205
Val Asp Asn Pro Ala Ser Phe Ala Asp Ser Met Leu Val Arg Ala Val
      210            215            220
Asn Tyr Asn Tyr Tyr Tyr Ser Leu Asn Ala Trp Leu Leu Leu Cys Pro
      225            230            235            240
Trp Trp Leu Cys Phe Asp Trp Ser Met Gly Cys Ile Pro Leu Ile Lys

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245	250	255
Ser Ile Ser Asp Trp Arg Val Ile Ala Leu Ala Ala Leu Trp Phe Cys		
260	265	270
Leu Ile Gly Leu Ile Cys Gln Ala Leu Cys Ser Glu Asp Gly His Lys		
275	280	285
Arg Arg Ile Leu Thr Leu Gly Leu Gly Phe Leu Val Ile Pro Phe Leu		
290	295	300
Pro Ala Ser Asn Leu Phe Phe Arg Val Gly Phe Val Val Ala Glu Arg		
305	310	315
Val Leu Tyr Leu Pro Ser Ile Gly Tyr Cys Val Leu Leu Thr Phe Gly		
325	330	335
Phe Gly Ala Leu Ser Lys His Thr Lys Lys Lys Lys Leu Ile Ala Ala		
340	345	350
Val Val Leu Gly Ile Leu Phe Ile Asn Thr Leu Arg Cys Val Leu Arg		
355	360	365
Ser Gly Glu Trp Arg Ser Glu Glu Gln Leu Phe Arg Ser Ala Leu Ser		
370	375	380
Val Cys Pro Leu Asn Ala Lys Val His Tyr Asn Ile Gly Lys Asn Leu		
385	390	395
Ala Asp Lys Gly Asn Gln Thr Ala Ala Ile Arg Tyr Tyr Arg Glu Ala		
405	410	415
Val Arg Leu Asn Pro Lys Tyr Val His Ala Met Asn Asn Leu Gly Asn		
420	425	430
Ile Leu Lys Glu Arg Asn Glu Leu Gln Glu Ala Glu Glu Leu Leu Ser		
435	440	445
Leu Ala Val Gln Ile Gln Pro Asp Phe Ala Ala Ala Trp Met Asn Leu		
450	455	460
Gly Ile Val Gln Asn Ser Leu Lys Arg Phe Glu Ala Ala Glu Gln Ser		
465	470	475
Tyr Arg Thr Ala Ile Lys His Arg Arg Lys Tyr Pro Asp Cys Tyr Tyr		
485	490	495
Asn Leu Gly Arg Leu Tyr Ala Asp Leu Asn Arg His Val Asp Ala Leu		
500	505	510
Asn Ala Trp Arg Asn Ala Thr Val Leu Lys Pro Glu His Ser Leu Ala		
515	520	525

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Trp Asn Asn Met Ile Ile Leu Leu Asp Asn Thr Gly Asn Leu Ala Gln
 530 535 540
 Ala Glu Ala Val Gly Arg Glu Ala Leu Glu Leu Ile Pro Asn Asp His
 545 550 555 560
 Ser Leu Met Phe Ser Leu Ala Asn Val Leu Gly Lys Ser Gln Lys Tyr
 565 570 575
 Lys Glu Ser Glu Ala Leu Phe Leu Lys Ala Ile Lys Ala Asn Pro Asn
 580 585 590
 Ala Ala Ser Tyr His Gly Asn Leu Ala Val Leu Tyr His Arg Trp Gly
 595 600 605
 His Leu Asp Leu Ala Lys Lys His Tyr Glu Ile Ser Leu Gln Leu Asp
 610 615 620
 Pro Thr Ala Ser Gly Thr Lys Glu Asn Tyr Gly Leu Leu Arg Arg Lys
 625 630 635 640
 Leu Glu Leu Met Gln Lys Lys Ala Val
 645

<210> 65

<211> 93

<212> PRT

<213> Homo sapiens

<400> 65

Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro Val Ala
 1 5 10 15
 Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe Tyr
 20 25 30
 Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu Pro
 35 40 45
 Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Ala Ser Leu Leu Ile
 50 55 60
 Val Gly Ala Val Phe Leu Cys Ala Arg Pro Arg Arg Ser Pro Ala Gln
 65 70 75 80
 Glu Asp Gly Lys Val Tyr Ile Asn Met Pro Gly Arg Gly
 85 90

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<210> 66

<211> 425

<212> PRT

<213> Homo sapiens

<400> 66

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Met Gly Ser Trp Ala Ala Val Asn Gly Ile Trp Val Glu Leu Pro Val
  1             5             10             15
Val Val Lys Glu Leu Pro Glu Gly Trp Ser Leu Pro Ser Tyr Val Ser
      20             25             30
Val Leu Val Ala Leu Gly Asn Leu Gly Leu Leu Val Val Thr Leu Trp
      35             40             45
Arg Arg Leu Ala Pro Gly Lys Asp Glu Gln Val Pro Ile Arg Val Val
      50             55             60
Gln Val Leu Gly Met Val Gly Thr Ala Leu Leu Ala Ser Leu Trp His
      65             70             75             80
His Val Ala Pro Val Ala Gly Gln Leu His Ser Val Ala Phe Leu Ala
      85             90             95
Leu Ala Phe Val Leu Ala Leu Ala Cys Cys Ala Ser Asn Val Thr Phe
      100            105            110
Leu Pro Phe Leu Ser His Leu Pro Pro Arg Phe Leu Arg Ser Phe Phe
      115            120            125
Leu Gly Gln Gly Leu Ser Ala Leu Leu Pro Cys Val Leu Ala Leu Val
      130            135            140
Gln Gly Val Gly Arg Leu Glu Cys Pro Pro Ala Pro Ile Asn Gly Thr
      145            150            155            160
Pro Gly Pro Pro Leu Asp Phe Leu Glu Arg Phe Pro Ala Ser Thr Phe
      165            170            175
Phe Trp Ala Leu Thr Ala Leu Leu Val Ala Ser Ala Ala Ala Phe Gln
      180            185            190
Gly Leu Leu Leu Leu Leu Pro Pro Pro Pro Ser Val Pro Thr Gly Glu
      195            200            205
Leu Gly Ser Gly Leu Gln Val Gly Ala Pro Gly Ala Glu Glu Glu Val
      210            215            220
Glu Glu Ser Ser Pro Leu Gln Glu Pro Pro Ser Gln Ala Ala Gly Thr
      225            230            235            240

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Thr Pro Gly Pro Asp Pro Lys Ala Tyr Gln Leu Leu Ser Ala Arg Ser
 245 250 255
 Ala Cys Leu Leu Gly Leu Leu Ala Ala Thr Asn Ala Leu Thr Asn Gly
 260 265 270
 Val Leu Pro Ala Val Gln Ser Phe Ser Cys Leu Pro Tyr Gly Arg Leu
 275 280 285
 Ala Tyr His Leu Ala Val Val Leu Gly Ser Ala Ala Asn Pro Leu Ala
 290 295 300
 Cys Phe Leu Ala Met Gly Val Leu Cys Arg Ser Leu Ala Gly Leu Gly
 305 310 315 320
 Gly Leu Ser Leu Leu Gly Val Phe Cys Gly Gly Tyr Leu Met Ala Leu
 325 330 335
 Ala Val Leu Ser Pro Cys Pro Pro Leu Val Gly Thr Ser Ala Gly Val
 340 345 350
 Val Leu Val Val Leu Ser Trp Val Leu Cys Leu Gly Val Phe Ser Tyr
 355 360 365
 Val Lys Val Ala Ala Ser Ser Leu Leu His Gly Gly Gly Arg Pro Ala
 370 375 380
 Leu Leu Ala Ala Gly Val Ala Ile Gln Val Gly Ser Leu Leu Gly Ala
 385 390 395 400
 Val Ala Met Phe Pro Pro Thr Ser Ile Tyr His Val Phe His Ser Arg
 405 410 415
 Lys Asp Cys Ala Asp Pro Cys Asp Ser
 420 425

<210> 67

<211> 149

<212> PRT

<213> Homo sapiens

<400> 67

Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn
 1 5 10 15
 Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr
 20 25 30
 Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile

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35 40 45
 Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp
 50 55 60
 Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn
 65 70 75 80
 Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met
 85 90 95
 Gly Gly Leu Gly Phe Ile Ile Leu Asp Arg Ser Asn Ala Pro Asn Ile
 100 105 110
 Pro Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val
 115 120 125
 Leu Leu Ser Phe Phe Met Ala Arg Val Phe Met Arg Met Lys Leu Pro
 130 135 140
 Gly Tyr Leu Met Gly
 145

<210> 68

<211> 396

<212> PRT

<213> Homo sapiens

<400> 68

Met Ala Met Ile Glu Leu Gly Phe Gly Arg Gln Asn Phe His Pro Leu
 1 5 10 15
 Lys Arg Lys Ser Ser Leu Leu Leu Lys Leu Ile Ala Val Val Phe Ala
 20 25 30
 Val Leu Leu Phe Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln
 35 40 45
 Cys Asn Trp Pro Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr
 50 55 60
 Thr Arg Glu Pro Val Leu Lys Ala Met Phe Leu Ala Asp Thr His Leu
 65 70 75 80
 Leu Gly Glu Phe Leu Gly His Trp Leu Asp Lys Leu Arg Arg Glu Trp
 85 90 95
 Gln Met Glu Arg Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu
 100 105 110

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Val Val Phe Ile Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr
 115 120 125
 Pro Glu Ala Trp Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg
 130 135 140
 His Pro Ser His Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile
 145 150 155 160
 Gly Phe His Tyr Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys
 165 170 175
 Val Phe Ser Ser Glu Arg Leu Phe Ser Trp Lys Gly Ile Asn Phe Val
 180 185 190
 Met Val Asn Ser Val Ala Leu Asn Gly Asp Gly Cys Gly Ile Cys Ser
 195 200 205
 Glu Thr Glu Ala Glu Leu Ile Glu Val Ser His Arg Leu Asn Cys Ser
 210 215 220
 Arg Glu Ala Arg Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro
 225 230 235 240
 Thr Ser Ala Pro Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser
 245 250 255
 Asp Ala Asn Cys Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp
 260 265 270
 Ile Pro Phe Lys Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln
 275 280 285
 Lys Leu Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr
 290 295 300
 His Ser Ala Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser
 305 310 315 320
 Val Pro Ser Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met
 325 330 335
 Gly Ser Ile Thr Pro Thr Asp Tyr Thr Leu Ser Lys Cys Tyr Leu Pro
 340 345 350
 Arg Glu Asp Val Val Leu Ile Ile Tyr Cys Gly Val Val Gly Phe Leu
 355 360 365
 Val Val Leu Thr Leu Thr His Phe Gly Leu Leu Ala Ser Pro Phe Leu
 370 375 380
 Ser Gly Leu Asn Leu Leu Gly Lys Arg Lys Thr Arg

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385

390

395

<210> 69

<211> 350

<212> PRT

<213> Homo sapiens

<400> 69

Met Ile Arg Gln Glu Arg Ser Thr Ser Tyr Gln Glu Leu Ser Glu Glu
 1 5 10 15
 Leu Val Gln Val Val Glu Asn Ser Glu Leu Ala Asp Glu Gln Asp Lys
 20 25 30
 Glu Thr Val Arg Val Gln Gly Pro Gly Ile Leu Pro Gly Leu Asp Ser
 35 40 45
 Glu Ser Ala Ser Ser Ser Ile Arg Phe Ser Lys Ala Cys Leu Lys Asn
 50 55 60
 Val Phe Ser Val Leu Leu Ile Phe Ile Tyr Leu Leu Leu Met Ala Val
 65 70 75 80
 Ala Val Phe Leu Val Tyr Arg Thr Ile Thr Asp Phe Arg Glu Lys Leu
 85 90 95
 Lys His Pro Val Met Ser Val Ser Tyr Lys Glu Val Asp Arg Tyr Asp
 100 105 110
 Ala Pro Gly Ile Ala Leu Tyr Pro Gly Gln Ala Gln Leu Leu Ser Cys
 115 120 125
 Lys His His Tyr Glu Val Ile Pro Pro Leu Thr Ser Pro Gly Gln Pro
 130 135 140
 Gly Asp Met Asn Cys Thr Thr Gln Arg Ile Asn Tyr Thr Asp Pro Phe
 145 150 155 160
 Ser Asn Gln Thr Val Lys Ser Ala Leu Ile Val Gln Gly Pro Arg Glu
 165 170 175
 Val Lys Lys Arg Glu Leu Val Phe Leu Gln Phe Arg Leu Asn Lys Ser
 180 185 190
 Ser Glu Asp Phe Ser Ala Ile Asp Tyr Leu Leu Phe Ser Ser Phe Gln
 195 200 205
 Glu Phe Leu Gln Ser Pro Asn Arg Val Gly Phe Met Gln Ala Cys Glu
 210 215 220

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Ser Ala Tyr Ser Ser Trp Lys Phe Ser Gly Gly Phe Arg Thr Trp Val
 225 230 235 240
 Lys Met Ser Leu Val Lys Thr Lys Glu Glu Asp Gly Arg Glu Ala Val
 245 250 255
 Glu Phe Arg Gln Glu Thr Ser Val Val Asn Tyr Ile Asp Gln Arg Pro
 260 265 270
 Ala Ala Lys Lys Ser Ala Gln Leu Phe Phe Val Val Phe Glu Trp Lys
 275 280 285
 Asp Pro Phe Ile Gln Lys Val Gln Asp Ile Val Thr Ala Asn Pro Trp
 290 295 300
 Asn Thr Ile Ala Leu Leu Cys Gly Ala Phe Leu Ala Leu Phe Lys Ala
 305 310 315 320
 Ala Glu Phe Ala Lys Leu Ser Ile Lys Trp Met Ile Lys Ile Arg Lys
 325 330 335
 Arg Tyr Leu Lys Arg Arg Gly Gln Ala Thr Ser His Ile Ser
 340 345 350

<210> 70

<211> 153

<212> PRT

<213> Homo sapiens

<400> 70

Met Thr Ile His Ile Leu Ile Leu Leu Leu Leu Ala Phe Ser Ala
 1 5 10 15
 Gln Gly Asp Leu Asp Thr Ala Ala Arg Arg Gly Gln His Gln Val Pro
 20 25 30
 Gln His Arg Gly His Val Cys Tyr Leu Gly Val Cys Arg Thr His Arg
 35 40 45
 Leu Ala Glu Ile Ile Tyr Trp Ile Arg Cys Leu His Gln Gly Ala Leu
 50 55 60
 Gly Glu Gly Gln Pro Arg Ala Pro Gly Pro Leu Gln Leu Trp Ala Pro
 65 70 75 80
 Pro Val Ala Arg Gly Gly Ser Pro Ala Arg Phe Pro Gly Phe Arg Pro
 85 90 95
 Ala Ala Arg Gly Leu Ala Gln Cys Pro Ala Arg Trp Val Thr Ser Gly

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100	105	110
Thr Ala Arg Pro Leu Leu Gly Phe Ser Leu Pro Ile Cys Met Leu Glu		
115	120	125
Leu Leu Leu His Ile Ser Ser Pro Leu Thr Pro Ala Pro Glu Thr Val		
130	135	140
Phe Pro Ser Pro Ser Pro Gly Cys Asp		
145	150	

<210> 71

<211> 1176

<212> DNA

<213> Homo sapiens

<400> 71

atggaggaggag tgagcgcgct gctggcccg	60
ggtggtcacgg cgtgcgcgcg gccggcggtg	120
ccaacgcaca cgatggtcaa ctgctgggtc	180
aaccgcaact gctgggactg tccccactgc	240
gactacaaca agccgatccc cgcccagtac	300
gcgcccagcc tgcgcgaccc ttgcgagccg	360
tgcaagaggt gcaaccacca ccagaccacc	420
cgcgaggagg gcaggtatga cgaggaggtc	480
tacaagctgt gccggccgtg ccaagcggt	540
cagctgcgcg ccctgttget cagccaccag	600
gcacagaact tctctccgc cgtgaagtcc	660
gccttcctgg cctgcgcctt cctactgacc	720
gcccaggca ccaactgtgcc cctggccctg	780
gacaatggca ccaccctgg gcccgagggc	840
cacatggcgg agaagctgtg tgaggcctgg	900
gtggcactgg gcctactcac ctgcctgctg	960
cggaggatcg atgccttctg cacctgcctg	1020
gagcagcacc tgcaggccgc ctcgcctagc	1080
tctttgtget gcctggttgg cttcacggcg	1140
cggaggttcc ggccccgaag gtcagagaag	1176

<210> 72

123/233

<211> 1491

<212> DNA

<213> Homo sapiens

<400> 72

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atggcgctgt ggcgcggtc cgcgtacgcg ggcttcctgg cgctggccgt gggctgcgtc      60
ttcctgctgg agccagagct gccaggctcg gcgctgcgct ctctctggag ctcgctgtgt      120
ctggggcccg cgctgcgcg cccgggaccc gtctcccccg agggccggtt ggcggcagcc      180
tgggacgcgc ttatcgtgcg gccagtcggy cgctggcgcc gcgtggcagt gggagtcagt      240
gcagtgtgtg atgtggtgct ctcaagggtg aagctcttgc aggcacttgg ccttagtcct      300
gggaatggga aagatcacag cattctgcgt tcaaggaatg atctggaaga agccttcatt      360
cacttcatgt ggaaggagc agctgctgag cgctctctca gtgataagga aacttttcac      420
gacattgccc aggttgcgtc agagtcccca ggagcccagc actatgtagg aggaaatgca      480
gctttaattg gacagaaatt tgcagccaac tcagatttaa aggttcttct ttgcggtcca      540
gttggcccaa ggctacatga gcttcttgat gacaatgtct ttgttccacc agagtcattg      600
caggaagtgg atgagttcca cctcatttta gagtatcaag caggggagga gtggggccag      660
ttaaaagctc cccatgccaa ccgattcacc ttctctcacc acctctccaa cggggccatg      720
aatatgctgg aggtgtttgt gtctagcctg gaggagtctc agccagacct ggtggtcctc      780
tctggattgc acatgatgga gggacaaaagc aaggagctcc agaggaagag actcttggag      840
gttgtaacct ccatttctga catccccaat ggtattccag ttcacctaga gctggccagt      900
atgactaaca gggagctcat gagcagcatt gtccatcagc aggtctttcc cgcggtgact      960
tcccttgggc tgaatgaaca ggagctgtta tttctcacc agtcagctc tggacctcac      1020
tcttctctct ctccctggaa cgggtgtcct gatgtgggca tggtcagtga catcctcttc      1080
tggtatcttg aagaacatgg gaggagtaaa agcagagcct cggatctcac caggatccat      1140
ttccacacgc tgggtctacca catcctggca actgtggatg gacactgggc caaccagctg      1200
gcagccgtgg ctgcaggagc tcgtgtggct gggacacagg cctgcgccac agaaaccata      1260
gacaccagcc gagtgtctct gagggcacc caagagttca tgacttccca ttcggaggca      1320
ggctccagga ttgtattaaa cccaacaag ccagtagtag aatggcacag agagggaata      1380
tccttccact tcacaccagt attggtgtgt aaagacccca ttogaactgt aggccttgga      1440
gatgccattt cagccgaagg actcttctat tcggaagta caccctcacta t      1491

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<210> 73

<211> 1251

<212> DNA

<213> Homo sapiens

<400> 73

124/233

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atgctggtgc atttatttcg ggtcgggatt cgggggtggc cattcccagg caggctgcta      60
ccgcccctcc gcttccagac attctcagct gtcaggtaact ctgatggcta cgcagctcc      120
tccctcctcc gggccgtggc ccacctgcgg tcccagctct gggcccacct ccctcgagcc      180
cccctagctc ccagatggag cccctctgcc tgggtgctggg ttgggggagc cctgctaggg      240
cccatggtae tgagtaagca tccccacctc tgecttgtgg ccctgtgtga ggcagaagag      300
gcccctcctg ccagctccac accccatgtc gtgggggtctc gotttaactg gaagctcttc      360
tggcagtttc tgcaccccca cctgctggtc ctgggggtag ccgtcgtgct ggccttgggt      420
gcggcactcg tgaatgtaca gatccccctg ctctctgggc agctggtaga ggtcgtggcc      480
aagtacacaa gggaccacgt agggagtttc atgactgagt cccagaatct cagcaccac      540
ctgcttatcc tctatggtgt ccagggaactg ctgacottcg ggtacctggt gctgctgtcc      600
cacgttgccg agcgcattggc tgtggacatg cggaggggcc tcttcagctc cctgctccgg      660
tactgccagc cgcagggtgc agagttagga caagacatca ccttctttga cgccaataag      720
acaggggcagc tggtagcccg cttgacaact gacgtgcagg agtttaagtc atccttcaag      780
cttgtcatct cccaggggct gcgaagctgc acccagggtg caggctgcct ggtgtccctg      840
tccatgctgt cgacacgcct cacgtgctg ctgatggtgg ccacaccagc cctgatggga      900
gtgggcaccc tgatgggctc aggcctccga aaattgtctt gccagtgtca ggagcagatc      960
gccagggcaa tgggcgtagc agacgaggcc ctgggcaatg tgcggactgt gctgctcttc     1020
gccatggagc aacgggaaga ggagcgctat ggggcagagc tggaaagcctg ccgctgccgg     1080
gcagaggagc tgggccgcgg catcgccctg ttccaagggc ttccaacat cgccttcaac     1140
tgcatggtct tgggtaccct atttattggg ggtcccttg tggccggaca gcagctgaca     1200
gggggagacc tcatgtcctt cctggtggcc tcccagacag tgcaaaggct g              1251

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<210> 74

<211> 1947

<212> DNA

<213> Homo sapiens

<400> 74

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atgattccta accagcataa tgctggagcc gggagccacc aacctgcagt tttcagaatg      60
gcctgtttgg acactgattt ggatcacatt cttccatctt ctgttcttcc tccattctgg      120
gctaagttag tagtgggacg ggttgccatt gtgtgttttg cacgcagcta tgatggagac      180
tttgtctttg atgactcaga agctattgtt aacaataagg ttgctggtgt tgcggccgt      240
gcagacctcc tgtgtgccct gttcttcttg ttatcttctc ttggctactg taaagcattt      300
agagaaagta acaaggaggg agcgcattct tccacctctc ggggtgctgt gagtatcttt      360
ctgggagcag tggccatgct gtgcaaagag caagggatca ctgtgctggg tttaaatgcg      420
gtatttgaca tottggtgat aggc aaatc aatgttctgg aaattgtcca gaaggtacta      480

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125/233

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<210> 75

<211> 279

<212> DNA

<213> Homo sapiens

<400> 75

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actccaggag agagatcctc actccctgcc ttttaccctg gcaattcagg ctcttgttcc 120
ggatgtgggt ccctctctct gccgctctg gcaggcctcg tggctgctga tgcggtgga 180
tcgtgctca tcgtgggggc ggtgttcctg tgcgcacgcc cagcccgag ccccgcccaa 240

126/233

gaagatggca aagtctacat caacatgccca ggcaggggc

279

<210> 76

<211> 1275

<212> DNA

<213> Homo sapiens

<400> 76

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ggtctgctgg	tggtagacct	ctggaggagg	ctggccccag	gaaaggacga	gcaggtcccc	180
atccgggtgg	tgcaggtgct	gggcatgggt	ggcacagccc	tgttgccctc	tctgtggcac	240
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ctggcactgg	catgctgtgc	ctcgaatgtc	actttctctg	ccttcttgag	ccacctgccca	360
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cctggccccc	cgtctgactt	ccttgagcgt	ttcccccga	gcaccttctt	ctgggcactg	540
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ctgtgtcttg	gcgtgttctc	ctacgtgaag	gtggcagcca	gtccctgct	gcattggcgg	1140
ggccggccgg	cattgctggc	agccggcggt	gccatccagg	tgggtctctc	gtcggcgct	1200
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<210> 77

<211> 447

<212> DNA

<213> Homo sapiens

<400> 77

127/233

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tacttctca tcaccggagg aataatttat gatgttattg ttgaacctcc aagtgtcgggt	180
tctatgactg atgaacatgg gcatcagagg ccagtagctt tcttggccta cagagtaaat	240
ggacaatata ttatggaagg acttgcaccc agcttctctat ttacaatggg aggttttaggt	300
ttcataatcc tggaccgatc gaatgcacca aatatcccaa aactcaatag attccttctt	360
ctgttcattg gattcgtctg tgcctattg agttttttca tggctagagt attcatgaga	420
atgaaactgc cgggctatct gatgggt	447

<210> 78

<211> 1188

<212> DNA

<213> Homo sapiens

<400> 78

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atctattact tagcgatctt tcagtgtaat tggcctgaag tgaaaaccac agcctctgat	180
ggtgaacaga ccacacgtga gcctgtgtc aaagccatgt ttttggctga caccattttg	240
cttggggaat tcctaggcca ctggctggac aaattacgaa gggaatggca gatggagaga	300
gogttccaga cagctctgtg gttgctgcag ccggaagtgc tcttcacctc gggggatata	360
tttgatgaag ggaagtggag caccctgag gcctggcgg atgatgtgga ggggtttcag	420
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ggcttccatt atgagatgaa cacatacaa gtagaacgct ttgagaaagt gttcagctct	540
gaaagactgt tttcttggaa aggcattaac tttgtgatgg tcaacagcgt ggcgtgaac	600
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tctggggaag acgtgctcc tgcagaggaa agggacatcc catttaagga gaactatgac	840
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agtggccaca cgcacagcgc ctgagagggt caccacgggg gccgagtcgc cgagctcagc	960
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cccacagact acaccctctc caagtgtac ctcccagctg aggatgtggt tttgatcacc	1080
tactgtggag tgggtggctt ccttgtggto ctcaactca ctcaacttgg gcttctagcc	1140
tcaccttttc tttctggtt gaacttgcct ggaaagcgtg agacaaga	1188

128/233

<210> 79

<211> 1050

<212> DNA

<213> Homo sapiens

<400> 79

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ggtatcttac caggcctgga cagcgagtcc gctccagca gcatccgctt cagcaaggcc      180
tgctgaaga acgtcttctc ggtcctactc atcttcatct acctgctgct catggctgtg      240
gccgtcttcc tggctctaccg gaccatcaca gactttctgt agaaactcaa gcacctgtc      300
atgtctgtgt ctacaagga agtggatcgc tatgatgccc caggatttgc cttgtacccc      360
ggtcaggccc agttgctcag ctgtaagcac cattaagagg tcattcctcc tctgacaagc      420
cctggccagc cgggtgacat gaattgcacc acccagagga toaactacac ggaccccttc      480
tccaatcaga ctgtgaaatc tgccctgatt gtccaggggc cccgggaagt gaaaaagcgg      540
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caggcctgtg agagtgccta ttccagctgg aagttctctg ggggcttcg cacctgggtc      720
aagatgtcac tggtaaagac caaggaggag gatgggcggg aagcagtgga gttccggcag      780
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gccaatcctt ggaacacaat tgctcttctc tgtggcgctt tcttggcatt atttaaagca      960
gcagagtttg ccaaactgag tataaaatgg atgatcaaaa ttagaaagag ataccttaaa     1020
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<210> 80

<211> 459

<212> DNA

<213> Homo sapiens

<400> 80

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ctgggcgtat gccggacca ccgcctggcg gagatcatat actggattcg ctgtctccac      180
caaggagccc tcggggaagg ccagccacga gcccaggac ccctacagct atgggcgccg      240
ccggtggcgc gaggcggaag cccggctcgg ttcccaggat tccggcctgc agcagggggg      300
ctagcgcagt gccagctcg ctgggtgacc tcgggcacgg ctctccct cctcggttc      360

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agtttgcta tctgtatgtt ggagcttcta ctccacattt cttctccct aactocagcc 420
 cctgaaaccg tottcccag tccctcccg ggetgagac 459

<210> 81

<211> 4027

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (192)...(1370)

<400> 81

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 gcccgctac ccgcctacc gcctaccgc ctacccccct gccggcctgc cgtcctcca 180
 cgcgagagc c atg gag gga gtg agc gcg ctg ctg gcc cgc tgc ccc acg 230
 Met Glu Gly Val Ser Ala Leu Leu Ala Arg Cys Pro Thr
 1 5 10
 gcc ggc ctg gcc ggc ggc ctg ggg gtc acg gcg tgc gcc gcg gcc ggc 278
 Ala Gly Leu Ala Gly Gly Leu Gly Val Thr Ala Cys Ala Ala Ala Gly
 15 20 25
 gtg ttg ctc tac cgg atc gcg cgg agg atg aag cca acg cac acg atg 326
 Val Leu Leu Tyr Arg Ile Ala Arg Arg Met Lys Pro Thr His Thr Met
 30 35 40 45
 gtc aac tgc tgg ttc tgc aac cag gat acg ctg gtg ccc tat ggg aac 374
 Val Asn Cys Trp Phe Cys Asn Gln Asp Thr Leu Val Pro Tyr Gly Asn
 50 55 60
 cgc aac tgc tgg gac tgt ccc cac tgc gag cag tac aac ggc ttc cag 422
 Arg Asn Cys Trp Asp Cys Pro His Cys Glu Gln Tyr Asn Gly Phe Gln
 65 70 75
 gag aac ggc gac tac aac aag ccg atc ccc gcc cag tac ttg gag cac 470
 Glu Asn Gly Asp Tyr Asn Lys Pro Ile Pro Ala Gln Tyr Leu Glu His
 80 85 90
 ctg aac cac gtg gtg agc agc gcg ccc agc ctg cgc gac cct tcg cag 518
 Leu Asn His Val Val Ser Ser Ala Pro Ser Leu Arg Asp Pro Ser Gln
 95 100 105

130/233

cag cag cag tgg gtg agc agc caa gtc ctg ctg tgc aag agg tgc aac	566
Pro Gln Gln Trp Val Ser Ser Gln Val Leu Leu Cys Lys Arg Cys Asn	
110 115 120 125	
cac cac cag acc acc aag atc aag cag ctg gcc gcc ttc gct ccc cgc	614
His His Gln Thr Thr Lys Ile Lys Gln Leu Ala Ala Phe Ala Pro Arg	
130 135 140	
gag gag ggc agg tat gac gag gag gtc gag gtg tac cgg cat cac ctg	662
Glu Glu Gly Arg Tyr Asp Glu Glu Val Glu Val Tyr Arg His His Leu	
145 150 155	
gag cag atg tac aag ctg tgc cgg ccg tgc caa gcg gct gtg gag tac	710
Glu Gln Met Tyr Lys Leu Cys Arg Pro Cys Gln Ala Ala Val Glu Tyr	
160 165 170	
tac atc aag cac cag aac cgc cag ctg cgc gcc ctg ttg ctc agc cac	758
Tyr Ile Lys His Gln Asn Arg Gln Leu Arg Ala Leu Leu Leu Ser His	
175 180 185	
cag ttc aag cgc cgg gag gcc gac cag acc cac gca cag aac ttc tcc	806
Gln Phe Lys Arg Arg Glu Ala Asp Gln Thr His Ala Gln Asn Phe Ser	
190 195 200 205	
tcc gcc gtg aag tcc ccg gtc cag gtc atc ctg ctc cgt gcc ctc gcc	854
Ser Ala Val Lys Ser Pro Val Gln Val Ile Leu Leu Arg Ala Leu Ala	
210 215 220	
ttc ctg gcc tgc gcc ttc cta ctg acc acc gcg ctg tat ggg gcc agc	902
Phe Leu Ala Cys Ala Phe Leu Leu Thr Thr Ala Leu Tyr Gly Ala Ser	
225 230 235	
gga cac ttc gcc cca gcc acc act gtg ccc ctg gcc ctg cca cct ggt	950
Gly His Phe Ala Pro Gly Thr Thr Val Pro Leu Ala Leu Pro Pro Gly	
240 245 250	
ggc aat ggc tca gcc aca cct gac aat ggc acc acc cct ggg gcc gag	998
Gly Asn Gly Ser Ala Thr Pro Asp Asn Gly Thr Thr Pro Gly Ala Glu	
255 260 265	
ggc tgg cgg cag ttg ctg ggc cta ctc ccc gag cac atg gcg gag aag	1046
Gly Trp Arg Gln Leu Leu Gly Leu Leu Pro Glu His Met Ala Glu Lys	
270 275 280 285	
ctg tgt gag gcc tgg gcc ttt ggg cag agc cac cag acg ggc gtc gtg	1094
Leu Cys Glu Ala Trp Ala Phe Gly Gln Ser His Gln Thr Gly Val Val	

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290	295	300	
gca ctg ggc cta ctc acc tgc ctg ctg gca atg ctg ctg gct ggc cgc			1142
Ala Leu Gly Leu Leu Thr Cys Leu Leu Ala Met Leu Leu Ala Gly Arg			
305	310	315	
atc agg ctc cgg agg atc gat gcc ttc tgc acc tgc ctg tgg gcc ctg			1190
Ile Arg Leu Arg Arg Ile Asp Ala Phe Cys Thr Cys Leu Trp Ala Leu			
320	325	330	
ctg ctg ggg ctg cac ctg gct gag cag cac ctg cag gcc gcc tgc cct			1238
Leu Leu Gly Leu His Leu Ala Glu Gln His Leu Gln Ala Ala Ser Pro			
335	340	345	
agc tgg cta gac acg ctc aag ttc agc acc aca tct ttg tgc tgc ctg			1286
Ser Trp Leu Asp Thr Leu Lys Phe Ser Thr Thr Ser Leu Cys Cys Leu			
350	355	360	
gtt ggc ttc acg gcg gct gtg gcc aca agg aag gca acg ggc cca cgg			1334
Val Gly Phe Thr Ala Ala Val Ala Thr Arg Lys Ala Thr Gly Pro Arg			
370	375	380	
agg ttc cgg ccc cga agg tca gag aag cag cca tgactgcggg ggg			1380
Arg Phe Arg Pro Arg Arg Ser Glu Lys Gln Pro			
385	390		
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tgctttt 4027

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<210> 82

<211> 2495

<212> DNA

<213> Homo sapiens

<220>

133/233

<221> CDS

<222> (30)...(1523)

<400> 82

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                               1           5

tac gcg ggc ttc ctg gcg ctg gcc gtg ggc tgc gtc ttc ctg ctg gag      101
Tyr Ala Gly Phe Leu Ala Leu Ala Val Gly Cys Val Phe Leu Leu Glu
      10           15           20

cca gag ctg cca ggc tcg gcg ctg cgc tct ctc tgg agc tcg ctg tgt      149
Pro Glu Leu Pro Gly Ser Ala Leu Arg Ser Leu Trp Ser Ser Leu Cys
      25           30           35           40

ctg ggg ccc gcg cct gcg ccc ccg gga ccc gtc tcc ccc gag ggc cgg      197
Leu Gly Pro Ala Pro Ala Pro Pro Gly Pro Val Ser Pro Glu Gly Arg
              45           50           55

ttg gcg gca gcc tgg gac gcg ctt atc gtg cgg cca gtc cgg cgc tgg      245
Leu Ala Ala Ala Trp Asp Ala Leu Ile Val Arg Pro Val Arg Arg Trp
              60           65           70

cgc cgc gtg gca gtg gga gtc aat gca tgt gtt gat gtg gtg ctc tca      293
Arg Arg Val Ala Val Gly Val Asn Ala Cys Val Asp Val Val Leu Ser
              75           80           85

ggg gtg aag ctc ttg cag gca ctt ggc ctt agt cct ggg aat ggg aaa      341
Gly Val Lys Leu Leu Gln Ala Leu Gly Leu Ser Pro Gly Asn Gly Lys
              90           95           100

gat cac agc att ctg cat tca agg aat gat ctg gaa gaa gcc ttc att      389
Asp His Ser Ile Leu His Ser Arg Asn Asp Leu Glu Glu Ala Phe Ile
      105           110           115           120

cac ttc atg tgg aag gga gca gct gct gag cgc ttc ttc agt gat aag      437
His Phe Met Trp Lys Gly Ala Ala Ala Glu Arg Phe Phe Ser Asp Lys
              125           130           135

gaa act ttt cac gac att gcc cag gtt gcg tca gag ttc cca gga gcc      485
Glu Thr Phe His Asp Ile Ala Gln Val Ala Ser Glu Phe Pro Gly Ala
              140           145           150

cag cac tat gta gga gga aat gca gct tta att gga cag aaa ttt gca      533
Gln His Tyr Val Gly Gly Asn Ala Ala Leu Ile Gly Gln Lys Phe Ala

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134/233

155	160	165	
gcc aac tca gat tta aag gtt ctt ctt tgc ggt cca gtt ggc cca agg			581
Ala Asn Ser Asp Leu Lys Val Leu Leu Cys Gly Pro Val Gly Pro Arg			
170	175	180	
cta cat gag ctt ctt gat gac aat gtc ttt gtt cca cca gag tca ttg			629
Leu His Glu Leu Leu Asp Asp Asn Val Phe Val Pro Pro Glu Ser Leu			
185	190	195	200
cag gaa gtg gat gag ttc cac ctc att tta gag tat caa gca ggg gag			677
Gln Glu Val Asp Glu Phe His Leu Ile Leu Glu Tyr Gln Ala Gly Glu			
205	210	215	
gag tgg ggc cag tta aaa gct ccc cat gcc aac cga ttc atc ttc tct			725
Glu Trp Gly Gln Leu Lys Ala Pro His Ala Asn Arg Phe Ile Phe Ser			
220	225	230	
cac gac ctc tcc aac ggg gcc atg aat atg ctg gag gtg ttt gtg tct			773
His Asp Leu Ser Asn Gly Ala Met Asn Met Leu Glu Val Phe Val Ser			
235	240	245	
agc ctg gag gag ttt cag cca gac ctg gtg gtc ctc tct gga ttg cac			821
Ser Leu Glu Glu Phe Gln Pro Asp Leu Val Val Leu Ser Gly Leu His			
250	255	260	
atg atg gag gga caa agc aag gag ctc cag agg aag aga ctc ttg gag			869
Met Met Glu Gly Gln Ser Lys Glu Leu Gln Arg Lys Arg Leu Leu Glu			
265	270	275	280
gtt gta acc tcc att tct gac atc ccc act ggt att cca gtt cac cta			917
Val Val Thr Ser Ile Ser Asp Ile Pro Thr Gly Ile Pro Val His Leu			
285	290	295	
gag ctg gcc agt atg act aac agg gag ctc atg agc agc att gtc cat			965
Glu Leu Ala Ser Met Thr Asn Arg Glu Leu Met Ser Ser Ile Val His			
300	305	310	
cag cag gtc ttt ccc gcg gtg act tcc ctt ggg ctg aat gaa cag gag			1013
Gln Gln Val Phe Pro Ala Val Thr Ser Leu Gly Leu Asn Glu Gln Glu			
315	320	325	
ctg tta ttt ctc acc cag tca gcc tct gga cct cac tct tct ctc tct			1061
Leu Leu Phe Leu Thr Gln Ser Ala Ser Gly Pro His Ser Ser Leu Ser			
330	335	340	
tcc tgg aac ggt gtt cct gat gtg ggc atg gtc agt gac atc ctc ttc			1109

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Ser Trp Asn Gly Val Pro Asp Val Gly Met Val Ser Asp Ile Leu Phe
 345 350 355 360
 tgg atc ttg aaa gaa cat ggg agg agt aaa agc aga gcc tcg gat ctc 1157
 Trp Ile Leu Lys Glu His Gly Arg Ser Lys Ser Arg Ala Ser Asp Leu
 365 370 375
 acc agg atc cat ttc cac acg ctg gtc tac cac atc ctg gca act gtg 1205
 Thr Arg Ile His Phe His Thr Leu Val Tyr His Ile Leu Ala Thr Val
 380 385 390
 gat gga cac tgg gcc aac cag ctg gca gcc gtg gct gca gga gct cgt 1253
 Asp Gly His Trp Ala Asn Gln Leu Ala Ala Val Ala Ala Gly Ala Arg
 395 400 405
 gtg gct ggg aca cag gcc tgc gcc aca gaa acc ata gac acc agc cga 1301
 Val Ala Gly Thr Gln Ala Cys Ala Thr Glu Thr Ile Asp Thr Ser Arg
 410 415 420
 gtg tct ctg agg gca ccc caa gag ttc atg act tcc cat tcg gag gca 1349
 Val Ser Leu Arg Ala Pro Gln Glu Phe Met Thr Ser His Ser Glu Ala
 425 430 435 440
 ggc tcc agg att gta tta aac cca aac aag cca gta gta gaa tgg cac 1397
 Gly Ser Arg Ile Val Leu Asn Pro Asn Lys Pro Val Val Glu Trp His
 445 450 455
 aga gag gga ata tcc ttc cac ttc aca cca gta ttg gtg tgt aaa gac 1445
 Arg Glu Gly Ile Ser Phe His Phe Thr Pro Val Leu Val Cys Lys Asp
 460 465 470
 ccc att cga act gta ggc ctt gga gat gcc att tca gcc gaa gga ctc 1493
 Pro Ile Arg Thr Val Gly Leu Gly Asp Ala Ile Ser Ala Glu Gly Leu
 475 480 485
 ttc tat tcg gaa gta cac cct cac tat taggaagatt cttaggggta 1540
 Phe Tyr Ser Glu Val His Pro His Tyr
 490 495
 atttttctga ggaaggagaa ctagccaact taagaattac aggaagaaag tggtttgaa 1600
 gacagocaaa gaaataaaaag cagattaaac tgtatcaggt acattccagc ctggttgcaa 1660
 ctccataaaa acatttcaga ttttaatccg aatttagcta atgagactgg atttttgttt 1720
 tttatgttgt gtgtcacaga gctaaaaact cagttcccaa atccccagtt tatgcagcgc 1780
 catcaggtat ttttaagctaa acttcttcac ccctgagagc atgtcagctg gagaaaaagca 1840
 gttcttcctt gcccaactga gaagtgcacg cccactcacc caacatcctg gtctctagga 1900

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aagcctcatg tgagggtcct cttctcttca gtcagtgcc catgggcaag gatcatgatt 1960
tccattccgt gttacaatga caatatttaa tgagcataac cttctcagtc tcttgetctc 2020
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gaaaggttca cgtggcccag gctgaacttc attgootagc tttggatgtg cttctgcca 2260
taaagactga tttttgttcg ttctgagcct tcaaggaatt tgttttttac aactggaata 2320
tgctcctgtg tgtgttaaca gatcatggat gttttatgtt ttcactgac atttaaagag 2380
tttgacctca gagctccagg atcatcagta aatttgcct gttatatatt tattttttta 2440
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<210> 83

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67)...(1320)

<400> 83

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gtcagc atg ctg gtg cat tta ttt cgg gtc ggg att cgg ggt ggc cca 108
Met Leu Val His Leu Phe Arg Val Gly Ile Arg Gly Gly Pro
1 5 10
ttc cca ggc agg ctg cta ccg ccc ctc cgc ttc cag aca ttc tca gct 156
Phe Pro Gly Arg Leu Leu Pro Pro Leu Arg Phe Gln Thr Phe Ser Ala
15 20 25 30
gtc agg tac tct gat ggc tac cgc agc tcc tcc ctc ctc cgg gcc gtg 204
Val Arg Tyr Ser Asp Gly Tyr Arg Ser Ser Ser Leu Leu Arg Ala Val
35 40 45
gcc cac ctg cgg tcc cag ctc tgg gcc cac ctc cct cga gcc ccc cta 252
Ala His Leu Arg Ser Gln Leu Trp Ala His Leu Pro Arg Ala Pro Leu
50 55 60
gct ccc aga tgg agc ccc tct gcc tgg tgc tgg gtt ggg gga gcc ctg 300
Ala Pro Arg Trp Ser Pro Ser Ala Trp Cys Trp Val Gly Gly Ala Leu
65 70 75

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cta ggc ccc atg gta ctg agt aag cat ccc cac ctc tgc ctt gtg gcc	348
Leu Gly Pro Met Val Leu Ser Lys His Pro His Leu Cys Leu Val Ala	
80 85 90	
ctg tgt gag gca gaa gag gcc cct cct gcc agc tcc aca ccc cat gtc	396
Leu Cys Glu Ala Glu Glu Ala Pro Pro Ala Ser Ser Thr Pro His Val	
95 100 105 110	
gtg ggg tct cgc ttt aac tgg aag ctc ttc tgg cag ttt ctg cac ccc	444
Val Gly Ser Arg Phe Asn Trp Lys Leu Phe Trp Gln Phe Leu His Pro	
115 120 125	
cac ctg ctg gtc ctg ggg gta gcc gtc gtg ctg gcc ttg ggt gcg gca	492
His Leu Leu Val Leu Gly Val Ala Val Val Leu Ala Leu Gly Ala Ala	
130 135 140	
ctc gtg aat gta cag atc ccc ctg ctc ctg gcc cag ctg gta gag gtc	540
Leu Val Asn Val Gln Ile Pro Leu Leu Leu Gly Gln Leu Val Glu Val	
145 150 155	
gtg gcc aag tac aca agg gac cac gta ggg agt ttc atg act gag tcc	588
Val Ala Lys Tyr Thr Arg Asp His Val Gly Ser Phe Met Thr Glu Ser	
160 165 170	
cag aat ctc agc acc cac ctg ctt atc ctc tat ggt gtc cag gga ctg	636
Gln Asn Leu Ser Thr His Leu Leu Ile Leu Tyr Gly Val Gln Gly Leu	
175 180 185 190	
ctg acc ttc ggg tac ctg gtg ctg ctg tcc cac gtt ggc gag cgc atg	684
Leu Thr Phe Gly Tyr Leu Val Leu Leu Ser His Val Gly Glu Arg Met	
195 200 205	
gct gtg gac atg cgg agg gcc ctc ttc agc tcc ctg ctc cgg tac tgc	732
Ala Val Asp Met Arg Arg Ala Leu Phe Ser Ser Leu Leu Arg Tyr Cys	
210 215 220	
cag ccg cag ggt gca gag ttg gga caa gac atc acc ttc ttt gac gcc	780
Gln Pro Gln Gly Ala Glu Leu Gly Gln Asp Ile Thr Phe Phe Asp Ala	
225 230 235	
aat aag aca ggg cag ctg gtg agc cgc ttg aca act gac gtg cag gag	828
Asn Lys Thr Gly Gln Leu Val Ser Arg Leu Thr Thr Asp Val Gln Glu	
240 245 250	
ttt aag tca tcc ttc aag ctt gtc atc tcc cag ggg ctg cga agc tgc	876
Phe Lys Ser Ser Phe Lys Leu Val Ile Ser Gln Gly Leu Arg Ser Cys	

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255	260	265	270	
acc cag gtg gca ggc tgc ctg gtg tcc ctg tcc atg ctg tcg aca cgc				924
Thr Gln Val Ala Gly Cys Leu Val Ser Leu Ser Met Leu Ser Thr Arg				
275	280	285		
ctc acg ctg ctg ctg atg gtg gcc aca cca gcc ctg atg gga gtg ggc				972
Leu Thr Leu Leu Leu Met Val Ala Thr Pro Ala Leu Met Gly Val Gly				
290	295	300		
acc ctg atg ggc tca ggc ctc cga aaa ttg tct tgc cag tgt cag gag				1020
Thr Leu Met Gly Ser Gly Leu Arg Lys Leu Ser Cys Gln Cys Gln Glu				
305	310	315		
cag atc gcc agg gca atg ggc gta gca gac gag gcc ctg ggc aat gtg				1068
Gln Ile Ala Arg Ala Met Gly Val Ala Asp Glu Ala Leu Gly Asn Val				
320	325	330		
cgg act gtg cgt gcc ttc gcc atg gag caa cgg gaa gag gag cgc tat				1116
Arg Thr Val Arg Ala Phe Ala Met Glu Gln Arg Glu Glu Glu Arg Tyr				
335	340	345	350	
ggg gca gag ctg gaa gcc tgc cgc tgc cgg gca gag gag ctg ggc cgc				1164
Gly Ala Glu Leu Glu Ala Cys Arg Cys Arg Ala Glu Glu Leu Gly Arg				
355	360	365		
ggc atc gcc ttg ttc caa ggg ctt tcc aac atc gcc ttc aac tgc atg				1212
Gly Ile Ala Leu Phe Gln Gly Leu Ser Asn Ile Ala Phe Asn Cys Met				
370	375	380		
gtc ttg ggt acc cta ttt att ggg ggc tcc ctt gtg gcc gga cag cag				1260
Val Leu Gly Thr Leu Phe Ile Gly Gly Ser Leu Val Ala Gly Gln Gln				
385	390	395		
ctg aca ggg gga gac ctc atg tcc ttc ctg gtg gcc tcc cag aca gtg				1308
Leu Thr Gly Gly Asp Leu Met Ser Phe Leu Val Ala Ser Gln Thr Val				
400	405	410		
caa agg ctg tgacattcca tgcattggaag gaccatcctt gacaggctgt gtg				1360
Gln Arg Leu				
415				
agctgccctt ccccatgcct gccacttcca gggatgacaa gctgacccct gtccccacac				1420
acccaccct tatagcttat tgctttgcgt tgggtccaaaa ccaccgctc agctgagcct				1480
ctgggatgac cagagctgat caccagacag ctcaaggcgg gctcccccc tccatatct				1540
ttccaagcta aacacaagca gttctacata aatatgttat ggtaaataat gagatagtaa				1600

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atatgctgta acagatc

1617

<210> 84

<211> 3269

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (260)...(2209)

<400> 84

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tagattcgag aagtggttta tcctttgact ggaaaagaaa agtagctgca gtattccccc      120
agcaacttgc gagagcatgc cgtatgccag gctgtgaggc togagagaca agcagtggaa      180
gagttgcggc ctgtttcatc tctggattgt aaatctgagc ctctttctgg cccctggaag      240
gggacagcat cacgatgga atg att cct aac cag cat aat gct gga gcc ggg      292
          Met Ile Pro Asn Gln His Asn Ala Gly Ala Gly
                1             5             10
agc cac caa cct gca gtt ttc aga atg gcc gtg ttg gac act gat ttg      340
Ser His Gln Pro Ala Val Phe Arg Met Ala Val Leu Asp Thr Asp Leu
                15             20             25
gat cac att ctt cca tct tct gtt ctt cct cca ttc tgg gct aag tta      388
Asp His Ile Leu Pro Ser Ser Val Leu Pro Pro Phe Trp Ala Lys Leu
                30             35             40
gta gtg gga tcg gtt gcc att gtg tgt ttt gca cgc agc tat gat gga      436
Val Val Gly Ser Val Ala Ile Val Cys Phe Ala Arg Ser Tyr Asp Gly
                45             50             55
gac ttt gtc ttt gat gac tca gaa gct att gtt aac aat aag gtt gct      484
Asp Phe Val Phe Asp Asp Ser Glu Ala Ile Val Asn Asn Lys Val Ala
                60             65             70             75
ggg gtt gtc ggc cgt gca gac ctc ctg tgt gcc ctg ttc ttc ttg tta      532
Gly Val Val Gly Arg Ala Asp Leu Leu Cys Ala Leu Phe Phe Leu Leu
                80             85             90
tct ttc ctt ggc tac tgt aaa gca ttt aga gaa agt aac aag gag gga      580
Ser Phe Leu Gly Tyr Cys Lys Ala Phe Arg Glu Ser Asn Lys Glu Gly
                95             100             105

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gcg cat tct tcc acc ttc tgg gtg ctg ctg agt atc ttt ctg gga gca	628
Ala His Ser Ser Thr Phe Trp Val Leu Leu Ser Ile Phe Leu Gly Ala	
110 115 120	
gtg gcc atg ctg tgc aaa gag caa ggg atc act gtg ctg ggt tta aat	676
Val Ala Met Leu Cys Lys Glu Gln Gly Ile Thr Val Leu Gly Leu Asn	
125 130 135	
gcg gta ttt gac atc ttg gtg ata ggc aaa ttc aat gtt ctg gaa att	724
Ala Val Phe Asp Ile Leu Val Ile Gly Lys Phe Asn Val Leu Glu Ile	
140 145 150 155	
gtc cag aag gta cta cat aag gac aag tca tta gag aat ctc ggc atg	772
Val Gln Lys Val Leu His Lys Asp Lys Ser Leu Glu Asn Leu Gly Met	
160 165 170	
ctc agg aac ggg ggc ctc ctc ttc aga atg acc ctg ctc acc tct gga	820
Leu Arg Asn Gly Gly Leu Leu Phe Arg Met Thr Leu Leu Thr Ser Gly	
175 180 185	
ggg gct ggg atg ctc tac gtg cgc tgg agg atc atg ggc acg ggc ccg	868
Gly Ala Gly Met Leu Tyr Val Arg Trp Arg Ile Met Gly Thr Gly Pro	
190 195 200	
ccg gcc ttc acc gag gtg gac aac ccg gcc tcc ttt gct gac agc atg	916
Pro Ala Phe Thr Glu Val Asp Asn Pro Ala Ser Phe Ala Asp Ser Met	
205 210 215	
ctg gtg agg gcc gta aac tac aat tac tac tat tca ttg aat gcc tgg	964
Leu Val Arg Ala Val Asn Tyr Asn Tyr Tyr Tyr Ser Leu Asn Ala Trp	
220 225 230 235	
ctg ctg ctg tgt ccc tgg tgg ctg tgt ttt gat tgg tca atg ggc tgc	1012
Leu Leu Leu Cys Pro Trp Trp Leu Cys Phe Asp Trp Ser Met Gly Cys	
240 245 250	
atc ccc ctc att aag tcc atc agc gac tgg agg gta att gca ctt gca	1060
Ile Pro Leu Ile Lys Ser Ile Ser Asp Trp Arg Val Ile Ala Leu Ala	
255 260 265	
gca ctc tgg ttc tgc cta att ggc ctg ata tgc caa gcc ctg tgc tct	1108
Ala Leu Trp Phe Cys Leu Ile Gly Leu Ile Cys Gln Ala Leu Cys Ser	
270 275 280	
gaa gac ggc cac aag aga agg atc ctt act ctg ggc ctg gga ttt ctc	1156
Glu Asp Gly His Lys Arg Arg Ile Leu Thr Leu Gly Leu Gly Phe Leu	

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285	290	295	
ggt atc cca ttt ctc ccc gcg agt aac ctg ttc ttc cga gtg ggc ttc			1204
Val Ile Pro Phe Leu Pro Ala Ser Asn Leu Phe Phe Arg Val Gly Phe			
300	305	310	315
gtg gtc gcg gag cgt gtc ctc tac ctc ccc agc att ggg tac tgt gtg			1252
Val Val Ala Glu Arg Val Leu Tyr Leu Pro Ser Ile Gly Tyr Cys Val			
320	325	330	
ctg ctg act ttt gga ttc gga gcc ctg agc aaa cat acc aag aaa aag			1300
Leu Leu Thr Phe Gly Phe Gly Ala Leu Ser Lys His Thr Lys Lys Lys			
335	340	345	
aaa ctc att gcc gct gtc gtg ctg gga atc tta ttc atc aac acg ctg			1348
Lys Leu Ile Ala Ala Val Val Leu Gly Ile Leu Phe Ile Asn Thr Leu			
350	355	360	
aga tgt gtg ctg cgc agc ggc gag tgg cgg agt gag gaa cag ctt ttc			1396
Arg Cys Val Leu Arg Ser Gly Glu Trp Arg Ser Glu Glu Gln Leu Phe			
365	370	375	
aga agt gct ctg tct gtg tgt ccc ctc aat gct aag gtt cac tac aac			1444
Arg Ser Ala Leu Ser Val Cys Pro Leu Asn Ala Lys Val His Tyr Asn			
380	385	390	395
att ggc aaa aac ctg gct gat aaa ggc aac cag aca gct gcc atc aga			1492
Ile Gly Lys Asn Leu Ala Asp Lys Gly Asn Gln Thr Ala Ala Ile Arg			
400	405	410	
tac tac cgg gaa gct gta aga tta aat ccc aag tat gtt cat gcc atg			1540
Tyr Tyr Arg Glu Ala Val Arg Leu Asn Pro Lys Tyr Val His Ala Met			
415	420	425	
aat aat ctt gga aat atc tta aaa gaa agg aat gag cta cag gaa gct			1588
Asn Asn Leu Gly Asn Ile Leu Lys Glu Arg Asn Glu Leu Gln Glu Ala			
430	435	440	
gag gag ctg ctg tct ttg gct gtt caa ata cag cca gac ttt gcc gct			1636
Glu Glu Leu Leu Ser Leu Ala Val Gln Ile Gln Pro Asp Phe Ala Ala			
445	450	455	
gcg tgg atg aat cta ggc ata gtg cag aat agc ctg aaa cgg ttt gaa			1684
Ala Trp Met Asn Leu Gly Ile Val Gln Asn Ser Leu Lys Arg Phe Glu			
460	465	470	475
gca gca gag caa agt tac cgg aca gca att aaa cac aga agg aaa tac			1732

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Ala Ala Glu Gln Ser Tyr Arg Thr Ala Ile Lys His Arg Arg Lys Tyr	
480 485 490	
cca gac tgt tac tac aac ctc ggg cgt ctg tat gca gat ctc aat cgc	1780
Pro Asp Cys Tyr Tyr Asn Leu Gly Arg Leu Tyr Ala Asp Leu Asn Arg	
495 500 505	
cac gtg gat gcc ttg aat gcg tgg aga aat gcc acc gtg ctg aaa cca	1828
His Val Asp Ala Leu Asn Ala Trp Arg Asn Ala Thr Val Leu Lys Pro	
510 515 520	
gag cac agc ctg gcc tgg aac aac atg att ata ctc ctc gac aat aca	1876
Glu His Ser Leu Ala Trp Asn Asn Met Ile Ile Leu Leu Asp Asn Thr	
525 530 535	
ggg aat tta gcc caa gct gaa gca gtt gga aga gag gca ctg gaa tta	1924
Gly Asn Leu Ala Gln Ala Glu Ala Val Gly Arg Glu Ala Leu Glu Leu	
540 545 550 555	
ata cct aat gat cac tct ctc atg ttc tgc ttg gca aac gtg ctg ggg	1972
Ile Pro Asn Asp His Ser Leu Met Phe Ser Leu Ala Asn Val Leu Gly	
560 565 570	
aaa tcc cag aaa tac aag gaa tct gaa gct tta ttc ctc aag gca att	2020
Lys Ser Gln Lys Tyr Lys Glu Ser Glu Ala Leu Phe Leu Lys Ala Ile	
575 580 585	
aaa gca aat cca aat gct gca agt tac cat ggt aat ttg gct gtg ctt	2068
Lys Ala Asn Pro Asn Ala Ala Ser Tyr His Gly Asn Leu Ala Val Leu	
590 595 600	
tat cat cgt tgg gga cat cta gac ttg gcc aag aaa cac tat gaa atc	2116
Tyr His Arg Trp Gly His Leu Asp Leu Ala Lys Lys His Tyr Glu Ile	
605 610 615	
tcc ttg cag ctt gac ccc acg gca tca gga act aag gag aat tac ggt	2164
Ser Leu Gln Leu Asp Pro Thr Ala Ser Gly Thr Lys Glu Asn Tyr Gly	
620 625 630 635	
ctg ctg aga aga aag cta gaa cta atg caa aag aaa gct gtc tgat	2210
Leu Leu Arg Arg Lys Leu Glu Leu Met Gln Lys Lys Ala Val	
640 645	
cctgtttcct tcatgttttg agtttgagtg tgtgtgtgca tgaggcatat cattaatagt	2270
atgtggttac atttaaccat ttaaaagtct tagacatggt attttactga tttttttota	2330
tgaaaacaaa gacatgcaaa aagattatag caccagcaat atactcttga atgcgtgata	2390

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tgatttttca ttgaaattgt attttttcag acaactcaaa tgtaattcta aaattccaaa 2450
 aatgtotttt ttaattaaac agaaaaagag aaaaaattat cttgagcaac ttttagtaga 2510
 attgagotta catttgggat ctgagccttg tcgtgtatgg actagcacta ttaaacttca 2570
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 tatattagca tttttattta atgacaaagc aaattaagtt tttttatctc ttttttttaa 2690
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 aggaagaaat tgactcttgc agtttttggg tgctctgact tgtgcaattt caatacacag 2870
 gagattatgt aatgtaatat ttttcataag cggttactat caattgaaag ttcaagccat 2930
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 aaacaatgtt ttgttttgtt cttctctgta tgctgttgac ctaatgattt atgcaatctc 3230
 tgtaatttct tatgcagtaa aattactaca caaactagc 3269

<210> 85

<211> 458

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (66)...(347)

<400> 85

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 Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro Val
 1 5 10 15
 gct gca gct cag acg act cca gga gag aga tca tca ctc cct gcc ttt 158
 Ala Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe
 20 25 30
 tac cct ggc act tca ggc tot tgt tcc gga tgt ggg tcc ctc tct ctg 206
 Tyr Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu
 35 40 45
 ccg ctc ctg gca ggc ctc gtg gct gct gat gcg gtg gca tcg ctg ctc 254

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Pro Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Ala Ser Leu Leu
50 55 60
atc gtg ggg gcg gtg ttc ctg tgc gca cgc cca cgc cgc agc ccc gcc 302
Ile Val Gly Ala Val Phe Leu Cys Ala Arg Pro Arg Arg Ser Pro Ala
65 70 75
caa gaa gat ggc aaa gtc tac atc aac atg cca ggc agg ggc tgaccc 350
Gln Glu Asp Gly Lys Val Tyr Ile Asn Met Pro Gly Arg Gly
80 85 90
tcctgcagct tggacotttg acttctgacc ctotcatact ggatgggtgtg tgggtggcaca 410
ggaacccccg ccccaacttt tggattgtaa taaaacaatt gaaacacc 458

<210> 86

<211> 1712

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (180)...(1457)

<400> 86

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tgggaaaaga actggetgtg acotttgccc tgacctggaa gggcccagcc ttgggtgaa 120
tggcagcacc cagcccgcc cgtccgtgtc tgacccaact gctggtgget ctcttcggc 179
atg ggc tcc tgg gct gcg gtc aat ggg atc tgg gtg gag cta cct gtg 227
Met Gly Ser Trp Ala Ala Val Asn Gly Ile Trp Val Glu Leu Pro Val
1 5 10 15
gtg gtc aaa gag ctt cca gag ggt tgg agc ctc ccc tct tac gtc tct 275
Val Val Lys Glu Leu Pro Glu Gly Trp Ser Leu Pro Ser Tyr Val Ser
20 25 30
gtg ctt gtg gct ctg ggg aac ctg ggt ctg ctg gtg gtg acc ctc tgg 323
Val Leu Val Ala Leu Gly Asn Leu Gly Leu Leu Val Val Thr Leu Trp
35 40 45
agg agg ctg gcc cca gga aag gac gag cag gtc ccc atc cgg gtg gtg 371
Arg Arg Leu Ala Pro Gly Lys Asp Glu Gln Val Pro Ile Arg Val Val
50 55 60
cag gtg ctg ggc atg gtg ggc aca gcc ctg ctg gcc tct ctg tgg cac 419

Gln Val Leu Gly Met Val Gly Thr Ala Leu Leu Ala Ser Leu Trp His			
65	70	75	80
cat gtg gcc cca gtg gca gga cag ttg cat tct gtg gcc ttc tta gca			467
His Val Ala Pro Val Ala Gly Gln Leu His Ser Val Ala Phe Leu Ala			
	85	90	95
ctg gcc ttt gtg ctg gca ctg gca tgc tgt gcc tcg aat gtc act ttc			515
Leu Ala Phe Val Leu Ala Leu Ala Cys Cys Ala Ser Asn Val Thr Phe			
	100	105	110
ctg ccc ttc ttg agc cac ctg cca cct cgc ttc tta cgg tca ttc ttc			563
Leu Pro Phe Leu Ser His Leu Pro Pro Arg Phe Leu Arg Ser Phe Phe			
	115	120	125
ctg ggt caa ggc ctg agt gcc ctg ctg ccc tgc gtg ctg gcc cta gtg			611
Leu Gly Gln Gly Leu Ser Ala Leu Leu Pro Cys Val Leu Ala Leu Val			
	130	135	140
cag ggt gtg ggc cgc ctc gag tgc ccg cca gcc ccc atc aac ggc acc			659
Gln Gly Val Gly Arg Leu Glu Cys Pro Pro Ala Pro Ile Asn Gly Thr			
145	150	155	160
cct ggc ccc ccg ctc gac ttc ctt gag cgt ttt ccc gcc agc acc ttc			707
Pro Gly Pro Pro Leu Asp Phe Leu Glu Arg Phe Pro Ala Ser Thr Phe			
	165	170	175
ttc tgg gca ctg act gcc ctt ctg gtc gct tca gct gct gcc ttc cag			755
Phe Trp Ala Leu Thr Ala Leu Leu Val Ala Ser Ala Ala Ala Phe Gln			
	180	185	190
ggt ctt ctg ctg ctg ttg ccg cca cca cca tct gta ccc aca ggg gag			803
Gly Leu Leu Leu Leu Leu Pro Pro Pro Pro Ser Val Pro Thr Gly Glu			
	195	200	205
tta gga tca ggc ctc cag gtg gga gcc cca gga gca gag gaa gag gtg			851
Leu Gly Ser Gly Leu Gln Val Gly Ala Pro Gly Ala Glu Glu Glu Val			
	210	215	220
gaa gag tcc tca cca ctg caa gag cca cca agc cag gca gca ggc acc			899
Glu Glu Ser Ser Pro Leu Gln Glu Pro Pro Ser Gln Ala Ala Gly Thr			
225	230	235	240
acc cct ggt cca gac cct aag gcc tat cag ctt cta tca gcc cgc agt			947
Thr Pro Gly Pro Asp Pro Lys Ala Tyr Gln Leu Leu Ser Ala Arg Ser			
	245	250	255

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gcc tgc ctg ctg ggc ctg ttg gcc gcc acc aac gcg ctg acc aat ggc	995
Ala Cys Leu Leu Gly Leu Leu Ala Ala Thr Asn Ala Leu Thr Asn Gly	
260 265 270	
gtg ctg cct gcc gtg cag agc ttt tcc tgc tta ccc tac ggg cgt ctg	1043
Val Leu Pro Ala Val Gln Ser Phe Ser Cys Leu Pro Tyr Gly Arg Leu	
275 280 285	
gcc tac cac ctg gct gtg gtg ctg ggc agt gct gcc aat ccc ctg gcc	1091
Ala Tyr His Leu Ala Val Val Leu Gly Ser Ala Ala Asn Pro Leu Ala	
290 295 300	
tgc ttc ctg gcc atg ggt gtg ctg tgc agg tcc ttg gca ggg ctg ggc	1139
Cys Phe Leu Ala Met Gly Val Leu Cys Arg Ser Leu Ala Gly Leu Gly	
305 310 315 320	
ggc ctc tct ctg ctg ggc gtg ttc tgt ggg ggc tac ctg atg gcg ctg	1187
Gly Leu Ser Leu Leu Gly Val Phe Cys Gly Gly Tyr Leu Met Ala Leu	
325 330 335	
gca gtc ctg agc ccc tgc ccg ccc ctg gtg ggc acc tcg gcg ggg gtg	1235
Ala Val Leu Ser Pro Cys Pro Pro Leu Val Gly Thr Ser Ala Gly Val	
340 345 350	
gtc ctc gtg gtg ctg tcg tgg gtg ctg tgt ctt ggc gtg ttc tcc tac	1283
Val Leu Val Val Leu Ser Trp Val Leu Cys Leu Gly Val Phe Ser Tyr	
355 360 365	
gtg aag gtg gca gcc agc tcc ctg ctg cat ggc ggg ggc cgg ccg gca	1331
Val Lys Val Ala Ala Ser Ser Leu Leu His Gly Gly Gly Arg Pro Ala	
370 375 380	
ttg ctg gca gcc ggc gtg gcc atc cag gtg ggc tct ctg ctc ggc gct	1379
Leu Leu Ala Ala Gly Val Ala Ile Gln Val Gly Ser Leu Leu Gly Ala	
385 390 395 400	
gtt gct atg ttc ccc ccg acc agc atc tat cac gtg ttc cac agc aga	1427
Val Ala Met Phe Pro Pro Thr Ser Ile Tyr His Val Phe His Ser Arg	
405 410 415	
aag gac tgt gca gac ccc tgt gac tcc tgagcctggg caggtgggga cccgcg	1480
Lys Asp Cys Ala Asp Pro Cys Asp Ser	
420 425	
tccccaacac ctgtctttcc ctcaatgtg ccaccatgcc tgagtgcctg cagcccagga	1540
ggcccgacaca ccggtacact cgtggacacc tacacactcc ataggagatc ctggtcttcc	1600

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aggggtgggca agggcaagga gcaggcttgg agccagggac cagtgggggc tgtagggtaa 1660
 gcccctgagc ctgggaccta catgtgggtt gcgtaataaa acatttgtat tt 1712

<210> 87

<211> 1055

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53)...(502)

<400> 87

accgggagge gcgtggggct tgaggccgag aacggccett gctgccacca ac atg 55

Met

1

gag act ttg tac cgt gtc ccg ttc tta gtg ctc gaa tgt ccc aac ctg 103

Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn Leu

5

10

15

aag ctg aag aag ccg ccc tgg ttg cac atg ccg tcg gcc atg act gtg 151

Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr Val

20

25

30

tat gct ctg gtg gtg gtg tct tac ttc ctc atc acc gga gga ata att 199

Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile Ile

35

40

45

tat gat gtt att gtt gaa cct cca agt gtc ggt tct atg act gat gaa 247

Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp Glu

50

55

60

65

cat ggg cat cag agg cca gta gct ttc ttg gcc tac aga gta aat gga 295

His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn Gly

70

75

80

caa tat att atg gaa gga ctt gca tcc agc ttc cta ttt aca atg gga 343

Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met Gly

85

90

95

ggg tta ggt ttc ata atc ctg gac cga tcg aat gca cca aat atc cca 391

Gly Leu Gly Phe Ile Ile Leu Asp Arg Ser Asn Ala Pro Asn Ile Pro

100

105

110

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aaa ctc aat aga ttc ctt ctt ctg ttc att gga ttc gtc tgt gtc cta 439
 Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val Leu
 115 120 125
 ttg agt ttt ttc atg gct aga gta ttc atg aga atg aaa ctg ccg ggc 487
 Leu Ser Phe Phe Met Ala Arg Val Phe Met Arg Met Lys Leu Pro Gly
 130 135 140 145
 tat ctg atg ggt tagagtgcct ttgagaagaa atcagtggat actggatttg c 540
 Tyr Leu Met Gly

tcctgtcaat gaagttttaaa aggctgtacc aatcctctaa tatgaaatgt ggaaaagaat 600
 gaagagcagc agtaaaagaa atatctagtg aaaaaacagg aagcgtattg aagcttggac 660
 tagaatttct tcttggtatt aaagagacaa gtttatcaca gaattttttt tcctgctggc 720
 ctattgctat accaatgatg ttgagtggca ttttcttttt agtttttcat taaaatatat 780
 tccatatcta caactataat atcaaataaa gtgattatgt tttacaacct tottaacatt 840
 ttttgagat gacatttctg attttcagaa attaacataa aatccagaag caagattccg 900
 taagctgaga actctggaca gttgatoagc tttacctatg gtgctttgcc ttttaactaga 960
 gtgtgtgatg gtagattatt tcagatatgt atgtaaaact gtttcctgaa caataagatg 1020
 tatgaacgga gcagaaataa atactttttc taatt 1055

<210> 88

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (222)...(1412)

<400> 88

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 gtgagaaaag cattctaata gctttattct gacatacgga ggtatggaga gcttgaagga 120
 gtcagagagg tgcccagcta agacctgaat gccatcacc tcccagggc totgcagttt 180
 tctcgtggtg aacccttgat ggatttggtg ttgcttgaga a atg gcg atg atc 233
 Met Ala Met Ile

1

gaa ttg ggg ttt gga aga cag aat ttt cat cca tta aag agg aag agt 281
 Glu Leu Gly Phe Gly Arg Gln Asn Phe His Pro Leu Lys Arg Lys Ser

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5	10	15	20	
tca ttg ctg ttg aaa ctc ata gct gtt gtc ttt gct gtg ctt cta ttt				329
Ser Leu Leu Leu Lys Leu Ile Ala Val Val Phe Ala Val Leu Leu Phe				
	25	30	35	
tgt gaa ttt tta atc tat tac tta gcg atc ttt cag tgt aat tgg cct				377
Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln Cys Asn Trp Pro				
	40	45	50	
gaa gtg aaa acc aca gcc tct gat ggt gaa cag acc aca cgt gag cct				425
Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr Thr Arg Glu Pro				
	55	60	65	
gtg ctc aaa gcc atg ttt ttg gct gac acc cat ttg ctt ggg gaa ttc				473
Val Leu Lys Ala Met Phe Leu Ala Asp Thr His Leu Leu Gly Glu Phe				
	70	75	80	
cta ggc cac tgg ctg gac aaa tta cga agg gaa tgg cag atg gag aga				521
Leu Gly His Trp Leu Asp Lys Leu Arg Arg Glu Trp Gln Met Glu Arg				
	85	90	95	100
gcg ttc cag aca gct ctg tgg ttg ctg cag ccg gaa gtc gtc ttc atc				569
Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu Val Val Phe Ile				
	105	110	115	
ctg ggg gat atc ttt gat gaa ggg aag tgg agc acc cct gag gcc tgg				617
Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr Pro Glu Ala Trp				
	120	125	130	
gcg gat gat gtg gag cgg ttt cag aaa atg ttc aga cac cca agt cat				665
Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg His Pro Ser His				
	135	140	145	
gta cag ctg aag gta gtt gct gga aac cat gac att ggc ttc cat tat				713
Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile Gly Phe His Tyr				
	150	155	160	
gag atg aac aca tac aaa gta gaa cgc ttt gag aaa gtg ttc agc tct				761
Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys Val Phe Ser Ser				
	165	170	175	180
gaa aga ctg ttt tct tgg aaa ggc att aac ttt gtg atg gtc aac agc				809
Glu Arg Leu Phe Ser Trp Lys Gly Ile Asn Phe Val Met Val Asn Ser				
	185	190	195	
gtg gcg ctg aac ggg gat ggc tgt ggc atc tgc tct gaa aca gaa gca				857

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Val Ala Leu Asn Gly Asp Gly Cys Gly Ile Cys Ser Glu Thr Glu Ala	
200 205 210	
gag ctc att gaa gtt tot cac aga ctg aac tgc tcc cga gag gca cgt	905
Glu Leu Ile Glu Val Ser His Arg Leu Asn Cys Ser Arg Glu Ala Arg	
215 220 225	
ggc tcc agc cgg tgt gga cct ggg cct ctg ctg ccc acg tct gcc cct	953
Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro Thr Ser Ala Pro	
230 235 240	
gtc ctc ctg cag cat tat cct ctg tat cgg aga agt gat gct aac tgt	1001
Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser Asp Ala Asn Cys	
245 250 255 260	
tct ggg gaa gac gct gct cct gca gag gaa agg gac atc cca ttt aag	1049
Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp Ile Pro Phe Lys	
265 270 275	
gag aac tat gac gtg ctt tca cgg gag gca tca caa aag ctg ctg tgg	1097
Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln Lys Leu Leu Trp	
280 285 290	
tgg ctc cag ccg cgc ctg gtt ctc agt ggc cac acg cac agc gcc tgc	1145
Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr His Ser Ala Cys	
295 300 305	
gag gtg cac cac ggg ggc cga gtc ccc gag ctc agc gtc cca tct ttc	1193
Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser Val Pro Ser Phe	
310 315 320	
agt tgg agg aac aga aac aac ccc agt ttc atc atg ggt agc atc acg	1241
Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met Gly Ser Ile Thr	
325 330 335 340	
ccc aca gac tac acc ctc tcc aag tgc tac ctc cca cgt gag gat gtg	1289
Pro Thr Asp Tyr Thr Leu Ser Lys Cys Tyr Leu Pro Arg Glu Asp Val	
345 350 355	
gtt ttg atc atc tac tgt gga gtg gtg ggc ttc ctt gtg gtc ctc aca	1337
Val Leu Ile Ile Tyr Cys Gly Val Val Gly Phe Leu Val Val Leu Thr	
360 365 370	
ctc act cac ttt ggg ctt cta gcc tca cct ttt ctt tct ggt ttg aac	1385
Leu Thr His Phe Gly Leu Leu Ala Ser Pro Phe Leu Ser Gly Leu Asn	
375 380 385	

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ttg ctc gga aag cgt aag aca aga tgaagagcag gcgccattat a 1430
 Leu Leu Gly Lys Arg Lys Thr Arg

390

395

aatatcaaag cccaagaaat ggaactttgg gcagagatca tgtagaatc aagtggatga 1490
 tgagaccaat tacaggccgt ctctctgcac agcacagaaa ttctcaatca ctgaaatgag 1550
 taactgcaaa ataaatagtt gattgtactg ttctcatgct ataaaagtgg acaggtactc 1610
 tacaac 1616

<210> 89

<211> 1860

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (69)...(1121)

<400> 89

gagaagtgtc ggtccgtgc gccgcccgtt gggcggtct caggtgtgcc gaagctotgg 60

tcagtgcc atg atc cgg cag gag cgc tcc aca tcc tac cag gag ctg 107

Met Ile Arg Gln Glu Arg Ser Thr Ser Tyr Gln Glu Leu

1

5

10

agt gag gag ttg gtc cag gtg gtt gag aac tca gag ctg gca gac gag 155

Ser Glu Glu Leu Val Gln Val Val Glu Asn Ser Glu Leu Ala Asp Glu

15

20

25

cag gac aag gag acg gtc aga gtc caa ggt ccg ggt atc tta cca ggc 203

Gln Asp Lys Glu Thr Val Arg Val Gln Gly Pro Gly Ile Leu Pro Gly

30

35

40

45

ctg gac agc gag tcc gcc tcc agc agc atc cgc ttc agc aag gcc tgc 251

Leu Asp Ser Glu Ser Ala Ser Ser Ser Ile Arg Phe Ser Lys Ala Cys

50

55

60

ctg aag aac gtc ttc tcg gtc cta ctc atc ttc atc tac ctg ctg ctc 299

Leu Lys Asn Val Phe Ser Val Leu Leu Ile Phe Ile Tyr Leu Leu Leu

65

70

75

atg gct gtg gcc gtc ttc ctg gtc tac cgg acc atc aca gac ttt cgt 347

Met Ala Val Ala Val Phe Leu Val Tyr Arg Thr Ile Thr Asp Phe Arg

80

85

90

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gag aaa ctc aag cac cct gtc atg tct gtg tct tac aag gaa gtg gat	395
Glu Lys Leu Lys His Pro Val Met Ser Val Ser Tyr Lys Glu Val Asp	
95 100 105	
cgc tat gat gcc cca ggt att gcc ttg tac ccc ggt cag gcc cag ttg	443
Arg Tyr Asp Ala Pro Gly Ile Ala Leu Tyr Pro Gly Gln Ala Gln Leu	
110 115 120 125	
ctc agc tgt aag cac cat tac gag gtc att cct cct ctg aca agc cct	491
Leu Ser Cys Lys His His Tyr Glu Val Ile Pro Pro Leu Thr Ser Pro	
130 135 140	
ggc cag ccg ggt gac atg aat tgc acc acc cag agg atc aac tac acg	539
Gly Gln Pro Gly Asp Met Asn Cys Thr Thr Gln Arg Ile Asn Tyr Thr	
145 150 155	
gac ccc ttc tcc aat cag act gtg aaa tct gcc ctg att gtc cag ggg	587
Asp Pro Phe Ser Asn Gln Thr Val Lys Ser Ala Leu Ile Val Gln Gly	
160 165 170	
ccc cgg gaa gtg aaa aag cgg gag ctg gtc ttc ctc cag ttc cgc ctg	635
Pro Arg Glu Val Lys Lys Arg Glu Leu Val Phe Leu Gln Phe Arg Leu	
175 180 185	
aac aag agt agt gag gac ttc agc gcc att gat tac ctc ctc ttc tct	683
Asn Lys Ser Ser Glu Asp Phe Ser Ala Ile Asp Tyr Leu Leu Phe Ser	
190 195 200 205	
tct ttc cag gag ttc ctg caa agc cca aac agg gta ggc ttc atg cag	731
Ser Phe Gln Glu Phe Leu Gln Ser Pro Asn Arg Val Gly Phe Met Gln	
210 215 220	
gcc tgt gag agt gcc tat tcc agc tgg aag ttc tct ggg ggc ttc cgc	779
Ala Cys Glu Ser Ala Tyr Ser Ser Trp Lys Phe Ser Gly Gly Phe Arg	
225 230 235	
acc tgg gtc aag atg tca ctg gta aag acc aag gag gag gat ggg cgg	827
Thr Trp Val Lys Met Ser Leu Val Lys Thr Lys Glu Glu Asp Gly Arg	
240 245 250	
gaa gca gtg gag ttc cgg cag gag aca agt gtg gtt aac tac att gac	875
Glu Ala Val Glu Phe Arg Gln Glu Thr Ser Val Val Asn Tyr Ile Asp	
255 260 265	
cag agg cca gct gcc aaa aaa agt gct caa ttg ttt ttt gtg gtc ttt	923
Gln Arg Pro Ala Ala Lys Lys Ser Ala Gln Leu Phe Phe Val Val Phe	

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270	275	280	285	
gaa tgg aaa gat cct ttc atc cag aaa gtc caa gat ata gtc act gcc				971
Glu Trp Lys Asp Pro Phe Ile Gln Lys Val Gln Asp Ile Val Thr Ala				
	290	295	300	
aat cct tgg aac aca att gct ctt ctc tgt ggc gcc ttc ttg gca tta				1019
Asn Pro Trp Asn Thr Ile Ala Leu Leu Cys Gly Ala Phe Leu Ala Leu				
	305	310	315	
ttt aaa gca gca gag ttt gcc aaa ctg agt ata aaa tgg atg atc aaa				1067
Phe Lys Ala Ala Glu Phe Ala Lys Leu Ser Ile Lys Trp Met Ile Lys				
	320	325	330	
att aga aag aga tac ctt aaa aga aga ggt cag gca acg agc cac ata				1115
Ile Arg Lys Arg Tyr Leu Lys Arg Arg Gly Gln Ala Thr Ser His Ile				
	335	340	345	
agc tgaagtcacc tcgcgttggt tagagaactg tccacatcaa tgggagctgt ca				1170
Ser				
350				
tcacttcac tttgtaaacy gagctatcaa caatcctgta ctcaactgaa gaaatggggc				1230
cttgctggga ggaacagcat gtaaaactgg aacttctaac cccgtcccaa aagaggcggc				1290
gtagagccta atagaagaga ctaattggata aacctacaag ttatttaaatt atttaaatta				1350
ttaataaact ttttaaagag ctggccaatg acttttgaat aggggtttgta gaagatgcct				1410
ttcttcctgt ttggttcatt gtattgtatt aggttaagct ctactagggt aatgaaggct				1470
ctacttttca ctttttaaaa gtggacaaaa gagtgtgatt ttctttttcc aaaaattcct				1530
gagtatcaag acgtgcaggt catgctttgg agcctatgca ctgtacacaa aggcacaaacc				1590
ctatgaacttt ggcacatctt gccattgatg tccagcctct gacatgctct ttgatttgtt				1650
aaatgttaaa tgagacttta aggtactag aaactagtaa ttaagtttct taatggactg				1710
agtagccacc tacttgctcg gctagaatgt ttgttgatgt atgagtttag attaacactc				1770
aaaagcacta ggacagatgt acatagaagg tgcctactca ttgtattttg atgatttcat				1830
taacaggtaa ataaaagta atacaaaagg				1860

<210> 90

<211> 783

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

154/233

<222> (245)...(706)

<400> 90

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gggaagtggg gactggccct ggtacctggc tccagagctg caccagagg cgatcagccc      180
ggtgcgggaa cggggcgggg tggccgcaac tacgggccac ggatcctgac ccgccctgcc      240
cacg atg act atc cac atc ctc atc ctg ctg ttg ctc ctc gcc ttc      286
Met Thr Ile His Ile Leu Ile Leu Leu Leu Leu Ala Phe
      1             5             10
tcc gcc caa ggg gac ctg gac act gca gcc agg cga ggc cag cac cag      334
Ser Ala Gln Gly Asp Leu Asp Thr Ala Ala Arg Arg Gly Gln His Gln
      15             20             25             30
gtc ccc cag cac cgc ggg cac gtc tgc tac ctg ggc gta tgc cgg acc      382
Val Pro Gln His Arg Gly His Val Cys Tyr Leu Gly Val Cys Arg Thr
      35             40             45
cac cgc ctg gcg gag atc ata tac tgg att cgc tgt ctc cac caa gga      430
His Arg Leu Ala Glu Ile Ile Tyr Trp Ile Arg Cys Leu His Gln Gly
      50             55             60
gcc ctc ggg gaa ggc cag cca cga gcc cca gga ccc cta cag cta tgg      478
Ala Leu Gly Glu Gly Gln Pro Arg Ala Pro Gly Pro Leu Gln Leu Trp
      65             70             75
gcg ccg ccg gtg gcg cga ggc gga agc ccg gct cgg ttc cca gga ttc      526
Ala Pro Pro Val Ala Arg Gly Gly Ser Pro Ala Arg Phe Pro Gly Phe
      80             85             90
cgg cct gca gcg agg ggg cta gcg cag tgc cca gct cgc tgg gtg acc      574
Arg Pro Ala Ala Arg Gly Leu Ala Gln Cys Pro Ala Arg Trp Val Thr
      95             100             105             110
tcg ggc acg gct cgt ccc ctc ctc ggc ttc agt ttg cct atc tgt atg      622
Ser Gly Thr Ala Arg Pro Leu Leu Gly Phe Ser Leu Pro Ile Cys Met
      115             120             125
ttg gag ctt cta ctc cac att tct tct ccc cta act cca gcc cct gaa      670
Leu Glu Leu Leu Leu His Ile Ser Ser Pro Leu Thr Pro Ala Pro Glu
      130             135             140
acc gtc ttc ccc agt ccc tcc ccg ggc tgc gac taggttgac ctagaag      720
Thr Val Phe Pro Ser Pro Ser Pro Gly Cys Asp

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145 150
 cacacgggac caggctgggc gaagaacact gacgccccaga gccgaataaa caagagttcc 780
 gtg 783

<210> 91

<211> 303

<212> PRT

<213> Homo sapiens

<400> 91

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 1 5 10 15
 Pro Gly Leu Glu Ala Val Pro Pro Val Ala Pro Pro Pro Ala Thr Ala
 20 25 30
 Ala Ser Gly Pro Ile Pro Lys Ser Gly Pro Glu Pro Lys Arg Arg His
 35 40 45
 Leu Gly Thr Leu Leu Gln Pro Thr Val Asn Lys Phe Ser Leu Arg Val
 50 55 60
 Phe Gly Ser His Lys Ala Val Glu Ile Glu Gln Glu Arg Val Lys Ser
 65 70 75 80
 Ala Gly Ala Trp Ile Ile His Pro Tyr Ser Asp Phe Arg Phe Tyr Trp
 85 90 95
 Asp Leu Ile Met Leu Leu Leu Met Val Gly Asn Leu Ile Val Leu Pro
 100 105 110
 Val Gly Ile Thr Phe Phe Lys Glu Glu Asn Ser Pro Pro Trp Ile Val
 115 120 125
 Phe Asn Val Leu Ser Asp Thr Phe Phe Leu Leu Asp Leu Val Leu Asn
 130 135 140
 Phe Arg Thr Gly Ile Val Val Glu Glu Gly Ala Glu Ile Leu Leu Ala
 145 150 155 160
 Pro Arg Ala Ile Arg Thr Arg Tyr Leu Arg Thr Trp Phe Leu Val Asp
 165 170 175
 Leu Ile Ser Ser Ile Pro Val Asp Tyr Ile Phe Leu Val Val Glu Leu
 180 185 190
 Glu Pro Arg Leu Asp Ala Glu Val Tyr Lys Thr Ala Arg Ala Leu Arg
 195 200 205

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Ile Val Arg Phe Thr Lys Ile Leu Ser Leu Leu Arg Leu Leu Arg Leu
 210 215 220
 Ser Arg Leu Ile Arg Tyr Ile His Gln Trp Glu Glu Ile Phe His Met
 225 230 235 240
 Thr Tyr Asp Leu Ala Ser Ala Val Val Arg Ile Phe Asn Leu Ile Gly
 245 250 255
 Met Met Leu Leu Leu Cys His Trp Asp Gly Cys Leu Gln Phe Leu Val
 260 265 270
 Pro Met Leu Gln Asp Phe Pro Pro Asp Cys Trp Val Ser Ile Asn His
 275 280 285
 Met Val Val Arg Ser Pro His Ser Ser Ala Phe Pro Gly Pro Ser
 290 295 300

<210> 92

<211> 283

<212> PRT

<213> Homo sapiens

<400> 92

Met Ala Asp Pro His Gln Leu Phe Asp Asp Thr Ser Ser Ala Gln Ser
 1 5 10 15
 Arg Gly Tyr Gly Ala Gln Arg Ala Pro Gly Gly Leu Ser Tyr Pro Ala
 20 25 30
 Ala Ser Pro Thr Pro His Ala Ala Phe Leu Ala Asp Pro Val Ser Asn
 35 40 45
 Met Ala Met Ala Tyr Gly Ser Ser Leu Ala Ala Gln Gly Lys Glu Leu
 50 55 60
 Val Asp Lys Asn Ile Asp Arg Phe Ile Pro Ile Thr Lys Leu Lys Tyr
 65 70 75 80
 Tyr Phe Ala Val Asp Thr Met Tyr Val Gly Arg Lys Leu Gly Leu Leu
 85 90 95
 Phe Phe Pro Tyr Leu His Gln Asp Trp Glu Val Gln Tyr Gln Gln Asp
 100 105 110
 Thr Pro Val Ala Pro Arg Phe Asp Val Asn Ala Pro Asp Leu Tyr Ile
 115 120 125
 Pro Ala Met Ala Phe Ile Thr Tyr Val Leu Val Ala Gly Leu Ala Leu

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130	135	140
Gly Thr Gln Asp Arg Phe Ser Pro Asp Leu Leu Gly Leu Gln Ala Ser		
145	150	155
Ser Ala Leu Ala Trp Leu Thr Leu Glu Val Leu Ala Ile Leu Leu Ser		
165	170	175
Leu Tyr Leu Val Thr Val Asn Thr Asp Leu Thr Thr Ile Asp Leu Val		
180	185	190
Ala Phe Leu Gly Tyr Lys Tyr Val Gly Met Ile Gly Gly Val Leu Met		
195	200	205
Gly Leu Leu Phe Gly Lys Ile Gly Tyr Tyr Leu Val Leu Gly Trp Cys		
210	215	220
Cys Val Ala Ile Phe Val Phe Met Ile Arg Thr Leu Arg Leu Lys Ile		
225	230	235
Leu Ala Asp Ala Ala Ala Glu Gly Val Pro Val Arg Gly Ala Arg Asn		
245	250	255
Gln Leu Arg Met Tyr Leu Thr Met Ala Val Ala Ala Ala Gln Pro Met		
260	265	270
Leu Met Tyr Trp Leu Thr Phe His Leu Val Arg		
275	280	

<210> 93

<211> 488

<212> PRT

<213> Homo sapiens

<400> 93

Met Ala Gly Lys Gly Ser Ser Gly Arg Arg Pro Leu Leu Leu Gly Leu
1 5 10 15
Leu Val Ala Val Ala Thr Val His Leu Val Ile Cys Pro Tyr Thr Lys
20 25 30
Val Glu Glu Ser Phe Asn Leu Gln Ala Thr His Asp Leu Leu Tyr His
35 40 45
Trp Gln Asp Leu Glu Gln Tyr Asp His Leu Glu Phe Pro Gly Val Val
50 55 60
Pro Arg Thr Phe Leu Gly Pro Val Val Ile Ala Val Phe Ser Ser Pro
65 70 75 80

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Ala Val Tyr Val Leu Ser Leu Leu Glu Met Ser Lys Phe Tyr Ser Gln
 85 90 95
 Leu Ile Val Arg Gly Val Leu Gly Leu Gly Val Ile Phe Gly Leu Trp
 100 105 110
 Thr Leu Gln Lys Glu Val Arg Arg His Phe Gly Ala Met Val Ala Thr
 115 120 125
 Met Phe Cys Trp Val Thr Ala Met Gln Phe His Leu Met Phe Tyr Cys
 130 135 140
 Thr Arg Thr Leu Pro Asn Val Leu Ala Leu Pro Val Val Leu Leu Ala
 145 150 155 160
 Leu Ala Ala Trp Leu Arg His Glu Trp Ala Arg Phe Ile Trp Leu Ser
 165 170 175
 Ala Phe Ala Ile Ile Val Phe Arg Val Glu Leu Cys Leu Phe Leu Gly
 180 185 190
 Leu Leu Leu Leu Leu Ala Leu Gly Asn Arg Lys Val Ser Val Val Arg
 195 200 205
 Ala Leu Arg His Ala Val Pro Ala Gly Ile Leu Cys Leu Gly Leu Thr
 210 215 220
 Val Ala Val Asp Ser Tyr Phe Trp Arg Gln Leu Thr Trp Pro Glu Gly
 225 230 235 240
 Lys Val Leu Trp Tyr Asn Thr Val Leu Asn Lys Ser Ser Asn Trp Gly
 245 250 255
 Thr Ser Pro Leu Leu Trp Tyr Phe Tyr Ser Ala Leu Pro Arg Gly Leu
 260 265 270
 Gly Cys Ser Leu Leu Phe Ile Pro Leu Gly Leu Val Asp Arg Arg Thr
 275 280 285
 His Ala Pro Thr Val Leu Ala Leu Gly Phe Met Ala Leu Tyr Ser Leu
 290 295 300
 Leu Pro His Lys Glu Leu Arg Phe Ile Ile Tyr Ala Phe Pro Met Leu
 305 310 315 320
 Asn Ile Thr Ala Ala Arg Gly Cys Ser Tyr Leu Leu Asn Asn Tyr Lys
 325 330 335
 Lys Ser Trp Leu Tyr Lys Ala Gly Ser Leu Leu Val Ile Gly His Leu
 340 345 350
 Val Val Asn Ala Ala Tyr Ser Ala Thr Ala Leu Tyr Val Ser His Phe

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355 360 365
 Asn Tyr Pro Gly Gly Val Ala Met Gln Arg Leu His Gln Leu Val Pro
 370 375 380
 Pro Gln Thr Asp Val Leu Leu His Ile Asp Val Ala Ala Ala Gln Thr
 385 390 395 400
 Gly Val Ser Arg Phe Leu Gln Val Asn Ser Ala Trp Arg Tyr Asp Lys
 405 410 415
 Arg Glu Asp Val Gln Pro Gly Thr Gly Met Leu Ala Tyr Thr His Ile
 420 425 430
 Leu Met Glu Ala Ala Pro Gly Leu Leu Ala Leu Tyr Arg Asp Thr His
 435 440 445
 Arg Val Leu Ala Ser Val Val Gly Thr Thr Gly Val Ser Leu Asn Leu
 450 455 460
 Thr Gln Leu Pro Pro Phe Asn Val His Leu Gln Thr Lys Leu Val Leu
 465 470 475 480
 Leu Glu Arg Leu Pro Arg Pro Ser
 485

<210> 94

<211> 182

<212> PRT

<213> Homo sapiens

<400> 94

Met Trp Pro Pro Asp Pro Asp Pro Asp Pro Asp Pro Glu Pro Ala Gly
 1 5 10 15
 Gly Ser Arg Pro Gly Pro Ala Val Pro Gly Leu Arg Ala Leu Leu Pro
 20 25 30
 Ala Arg Ala Phe Leu Cys Ser Leu Lys Gly Arg Leu Leu Leu Ala Glu
 35 40 45
 Ser Gly Leu Ser Phe Ile Thr Phe Ile Cys Tyr Val Ala Ser Ser Ala
 50 55 60
 Ser Ala Phe Leu Thr Ala Pro Leu Leu Glu Phe Leu Leu Ala Leu Tyr
 65 70 75 80
 Phe Leu Phe Ala Asp Ala Met Gln Leu Asn Asp Lys Trp Gln Gly Leu
 85 90 95

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Cys Trp Pro Met Met Asp Phe Leu Arg Cys Val Thr Ala Ala Leu Ile
 100 105 110
 Tyr Phe Ala Ile Ser Ile Thr Ala Ile Ala Lys Tyr Ser Asp Gly Ala
 115 120 125
 Ser Lys Ala Ala Gly Val Phe Gly Phe Phe Ala Thr Ile Val Phe Ala
 130 135 140
 Thr Asp Phe Tyr Leu Ile Phe Asn Asp Val Ala Lys Phe Leu Lys Gln
 145 150 155 160
 Gly Asp Ser Ala Asp Glu Thr Thr Ala His Lys Thr Glu Glu Glu Asn
 165 170 175
 Ser Asp Ser Asp Ser Asp
 180

<210> 95

<211> 184

<212> PRT

<213> Homo sapiens

<400> 95

Met Asp Gly Leu Arg Gln Arg Val Glu His Phe Leu Glu Gln Arg Asn
 1 5 10 15
 Leu Val Thr Glu Val Leu Gly Ala Leu Glu Ala Lys Thr Gly Val Glu
 20 25 30
 Lys Arg Tyr Leu Ala Ala Gly Ala Val Thr Leu Leu Ser Leu Tyr Leu
 35 40 45
 Leu Phe Gly Tyr Gly Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe Val
 50 55 60
 Tyr Pro Ala Tyr Ala Ser Ile Lys Ala Ile Glu Ser Pro Ser Lys Asp
 65 70 75 80
 Asp Asp Thr Val Trp Leu Thr Tyr Trp Val Val Tyr Ala Leu Phe Gly
 85 90 95
 Leu Ala Glu Phe Phe Ser Asp Leu Leu Leu Ser Trp Phe Pro Phe Tyr
 100 105 110
 Tyr Val Gly Lys Cys Ala Phe Leu Leu Phe Cys Met Ala Pro Arg Pro
 115 120 125
 Trp Asn Gly Ala Leu Met Leu Tyr Gln Arg Val Val Arg Pro Leu Phe

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130 135 140
 Leu Arg His His Gly Ala Val Asp Arg Ile Met Asn Asp Leu Ser Gly
 145 150 155 160
 Arg Ala Leu Asp Ala Ala Ala Gly Ile Thr Arg Asn Val Lys Pro Ser
 165 170 175
 Gln Thr Pro Gln Pro Lys Asp Lys
 180

<210> 96

<211> 140

<212> PRT

<213> Homo sapiens

<400> 96

Met Ser Arg Phe Leu Asn Val Leu Arg Ser Trp Leu Val Met Val Ser
 1 5 10 15
 Ile Ile Ala Met Gly Asn Thr Leu Gln Ser Phe Arg Asp His Thr Phe
 20 25 30
 Leu Tyr Glu Lys Leu Tyr Thr Gly Lys Pro Asn Leu Val Asn Gly Leu
 35 40 45
 Gln Ala Arg Thr Phe Gly Ile Trp Thr Leu Leu Ser Ser Val Ile Arg
 50 55 60
 Cys Leu Cys Ala Ile Asp Ile His Asn Lys Thr Leu Tyr His Ile Thr
 65 70 75 80
 Leu Trp Thr Phe Leu Leu Ala Leu Gly His Phe Leu Ser Glu Leu Phe
 85 90 95
 Val Tyr Gly Thr Ala Ala Pro Thr Ile Gly Val Leu Ala Pro Leu Met
 100 105 110
 Val Ala Ser Phe Ser Ile Leu Gly Met Leu Val Gly Leu Arg Tyr Leu
 115 120 125
 Glu Val Glu Pro Val Ser Arg Gln Lys Lys Arg Asn
 130 135 140

<210> 97

<211> 153

<212> PRT

162/233

<213> Homo sapiens

<400> 97

Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg Val
 1 5 10 15
 Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly Leu
 20 25 30
 Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val Ala
 35 40 45
 Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe Leu
 50 55 60
 His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
 65 70 75 80
 Arg Leu Leu Thr His Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe Thr
 85 90 95
 Ser Ser Arg Lys Phe Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe Leu
 100 105 110
 Ala Ser Phe Tyr Thr Lys Tyr Asp Pro Thr His Phe Ile Leu Asn Thr
 115 120 125
 Ala Ser Leu Leu Ser Val Leu Ile Pro Lys Met Pro Gln Leu His Gly
 130 135 140
 Val Arg Ile Phe Gly Ile Asn Lys Tyr
 145 150

<210> 98

<211> 173

<212> PRT

<213> Homo sapiens

<400> 98

Met Ala Ala Phe Leu Ile Gln Thr Lys Asp Asn Pro Met Lys Ala Val
 1 5 10 15
 Gly Val Leu Ala Gly Thr Met Ala Thr Val Val Ala Ile Thr Val Leu
 20 25 30
 Ile Ser Thr Ala Thr Phe Trp Arg Asn Lys Lys Ser Asn Lys Val Leu
 35 40 45
 Pro Met Arg Arg Val Leu Arg Lys Arg Pro Ser Pro Ala Pro Arg Thr

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50 55 60
 Ile Arg Ile Glu Trp Leu Lys Ser Lys Ser Thr Lys Ala Ala Thr Lys
 65 70 75 80
 Phe Met Leu Lys Glu Lys Pro Pro Asn Glu Asn Cys Asn Asn Asn Ser
 85 90 95
 Pro Glu Ser Ser Leu Leu Pro Arg Ala Pro Ala Leu Pro Pro Pro Pro
 100 105 110
 Ser Val Ala Pro Ser Thr Gly Ala Ala Gln Trp Thr Val Pro Thr Val
 115 120 125
 Ser Gly Ser Leu Thr Pro Gln Pro Thr Gln Pro Pro Pro Lys Pro Lys
 130 135 140
 Thr Met Gly Ser Pro Val Gln Ser Thr Leu Ile Ser Glu Leu Lys Gln
 145 150 155 160
 Lys Phe Glu Lys Lys Ser Val His Asn Lys Ala Tyr Phe
 165 170

<210> 99

<211> 75

<212> PRT

<213> Homo sapiens

<400> 99

Met Ile Gly Asp Ile Leu Leu Phe Gly Thr Leu Leu Met Asn Ala Gly
 1 5 10 15
 Ala Val Leu Asn Phe Lys Leu Lys Lys Lys Asp Thr Gln Gly Phe Gly
 20 25 30
 Glu Glu Ser Arg Glu Pro Ser Thr Gly Asp Asn Ile Arg Glu Phe Leu
 35 40 45
 Leu Ser Leu Arg Tyr Phe Arg Ile Phe Ile Ala Leu Trp Asn Ile Phe
 50 55 60
 Met Met Phe Cys Met Ile Val Leu Phe Gly Ser
 65 70 75

<210> 100

<211> 159

<212> PRT

164/233

<213> Homo sapiens

<400> 100

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Met Glu Leu Pro Ala Val Asn Leu Lys Val Ile Leu Leu Gly His Trp
  1             5             10             15
Leu Leu Thr Thr Trp Gly Cys Ile Val Phe Ser Gly Ser Tyr Ala Trp
          20             25             30
Ala Asn Phe Thr Ile Leu Ala Leu Gly Val Trp Ala Val Ala Gln Arg
          35             40             45
Asp Ser Ile Asp Ala Ile Ser Met Phe Leu Gly Gly Leu Leu Ala Thr
          50             55             60
Ile Phe Leu Asp Ile Val His Ile Ser Ile Phe Tyr Pro Arg Val Ser
          65             70             75             80
Leu Thr Asp Thr Gly Arg Phe Gly Val Gly Met Ala Ile Leu Ser Leu
          85             90             95
Leu Leu Lys Pro Leu Ser Cys Cys Phe Val Tyr His Met Tyr Arg Glu
          100             105             110
Arg Gly Gly Glu Leu Leu Val His Thr Gly Phe Leu Gly Ser Ser Gln
          115             120             125
Asp Arg Ser Ala Tyr Gln Thr Ile Asp Ser Ala Glu Ala Pro Ala Asp
          130             135             140
Pro Phe Ala Val Pro Glu Gly Arg Ser Gln Asp Ala Arg Gly Tyr
          145             150             155

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<210> 101

<211> 909

<212> DNA

<213> Homo sapiens

<400> 101

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atggaggcag agcagcggcc ggcggcgggg gccagcgaag gggcgacccc tggactggag      60
gcggtgcctc ccgttgctcc ccgcctgcg accgcggcct caggtccgat ccccaaatct      120
gggcctgagc ctaagaggag gcacctggg acgtgctcc agcctacggt caacaagttc      180
tcccttcggg tgttcggcag ccacaaagca gtggaatcg agcaggagcg ggtgaagtca      240
gcgggggcct ggatcatcca cccctacagc gacttcgggt ttactggga cctgatcatg      300
ctgctgctga tggtagggaa cctcatcgtc ctgcctgtgg gcacacctt cttcaaggag      360
gagaactccc cgccttgat cgtcttcaac gtattgtctg atactttctt cctactggat      420

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ctggtgctca acttccgaac gggcatcgtg gtggaggagg gtgctgagat cctgctggca 480
 ccgcggggcca tccgcacgcg ctacctgcgc acctggttcc tggttgacct catctottct 540
 atccctgtgg attacatctt cctagtgggtg gagctggagc cacggttgga cgtgagggtc 600
 tacaaaacgg cacggggcct acgcacgtt cgcttcacca agatcctaag cctgctgagg 660
 ctgtcccgcc totcccgct catccgtac atacaccagt gggaggagat ctttcacatg 720
 acctatgacc tggccagtgc tgtggttcgc atottcaacc tcattgggat gatgctgctg 780
 ctatgtcact gggatggctg tctgcagttc ctggtgccca tgetgcagga cttccctccc 840
 gactgctggg tctccatcaa ccacatgggtg gtgagaagtc cccacagctc tgcttttctt 900
 gggcctttct 909

<210> 102

<211> 849

<212> DNA

<213> Homo sapiens

<400> 102

atggccgacc cccaccagct ttctgatgac acaagttcag cccagagccg gggctatggg 60
 gccacagcggg cacctgggtg cctgagttat cctgcagcct ctcccacgac ccatgcagcc 120
 ttcttggtcg acccgggtgc caacatggcc atggcctatg ggagcagcct ggccgcgcag 180
 ggcaaggagc tgggtggataa gaacatcgac cgcttcatcc ccatcaccaa gctcaagtat 240
 tacttttctg tggacaccat gtatgtgggc agaaagctgg gctgctgtt cttcccctac 300
 ctacaccagg actgggaagt gcagtaacca caggacaccc cgggtggccc ccgctttgac 360
 gtcaatgcc cggacctcta cattccagca atggctttca tcacctacgt tttggtggct 420
 ggtcttgctc tggggaccca ggataggttc tcccagacc tcttggggct gcaagcgagc 480
 tcagccctgg cctggctgac cctggaggtg ctggccatcc tgetcagcct ctatctggtc 540
 actgtcaaca ccgacctac caccatcgac ctggtggcct tcttgggcta caaatatgtc 600
 gggatgattg gcggggctct catgggcctg ctotctggga agattggcta ctacctggtg 660
 ctgggctggt gctgcgtagc catotttgtg ttcattgatcc ggacgctgcg gctgaagatc 720
 ttggcagacg cagcagctga gggggctccc gtgcgtgggg cccggaacca gctgcgcagt 780
 tacctgacca tggcgggtggc ggcggcgag cctatgctca tgtactggct caccttccac 840
 ctggtgcgg 849

<210> 103

<211> 1464

<212> DNA

<213> Homo sapiens

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<400> 103

atggctggaa aggggtcatc aggcaggcgg cccctgctgc tggggctgct ggtggccgta	60
gccactgtcc acctggcatc ctgtccctac accaaagtgg aggagagctt caacctgcag	120
gccacacatg acctgctcta ccactggcaa gacctggagc agtacgacca tcttgagttc	180
cccgagtcg tcccaggac gttcctcggg ccagtgggta tcgcagtgtt ctccagcccc	240
gcggtttacg tgctttcgtt gttagaaatg tccaagtttt actctcagct aatagttaga	300
ggagtgcctt gactcggcgt gatttttgga ctctggacgt tacaaaagga agtgagacgg	360
cacttcgggg ccattggtggc caccatgttc tgctgggtga cggccatgca gttccacctg	420
atgtttctact gcacgcggac actgcccatt gtgctggccc tgctgtagt cctgtggccc	480
ctcgcggcct ggctgcggca cgagtgggcc cgcttcatct ggctgtcagc ctccgccatc	540
atcgtgttca ggggtggagct gtgcctgttc ctgggcctcc tgctgtgctt ggccttgggc	600
aaccgaaagg tttctgtagt cagagccctt cgccacggcg tcccggcagg gatcctctgt	660
ttaggactga cggttgctgt ggactcttat ttttggcggc agctcacttg gccggaagga	720
aaggtgcttt ggtacaacac tgtcctgaac aaaagctcca actgggggac ctccccgctg	780
ctgtggtact tctactcagc cctgccccgc ggcttgggtt gcagcctgct ctccatcccc	840
ctgggcttgg tagacagaag gacgcacgcg ccgacgggtg tggcactggg ctccatggca	900
ctctactccc tcttgcacaa caaggagcta cgcttcatca tctatgcctt ccccatgctc	960
aacatcacgg ctgccagagg ctgctcctac ctgctgaata actataaaaa gtcttgggtg	1020
tacaaagcag ggtctctgct tgtgatcgga cacctcgtgg tgaatgccgc ctactcagcc	1080
acggccctgt atgtgtccca tttcaactac ccagggtggcg tcgcaatgca gaggctgcac	1140
cagctggtgc cccccagac agacgtcctt ctgcacattg acgtggcagc cggccagaca	1200
ggtgtgtctc ggtttctcca agtcaacagc gcctggaggt acgacaagag ggaggatgtg	1260
cagccgggga caggcatgct ggcatacaca cacatcctca tggaggcggc ccctgggctc	1320
ctggccctct acagggaac acaccgggtc ctggccagcg tcgtggggac cacagggtgtg	1380
agtctgaacc tgaccacaact gcccccttc aacgtccacc tgcagacaaa gctggtgctt	1440
ctggagaggg tccccggcc gtcc	1464

<210> 104

<211> 546

<212> DNA

<213> Homo sapiens

<400> 104

atgtggcccc cagacccccga ccccgaccgg gaccccgagc ctgccggcgg ctcccgctcc	60
ggccccgcgg tccccgggct ccgcgcctgt ctgccggcgc gggctttcct ctgctctctc	120
aaaggccgcc tcttgetggc cgagtcgggt ctctcattea tcacttttat ctgctatgtg	180

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gcgtcctcag catctgcctt cctcacagcg cctctgctgg agttcctgct ggccctgtac 240
 ttctctcttg ctgatgccat gcagctgaat gacaagtggc agggcttgtg ctggcccatg 300
 atggacttcc tgcgctgtgt caccggggcc ctcatctact ttgctatctc catcacggcc 360
 atcgccaagt actcggatgg ggcttccaaa gccgctgggg tgtttggctt ctttgcctac 420
 atcgtgtttg caactgattt ctacctgac tttacgacg tggccaaatt cctcaaacia 480
 ggggactctg cagatgagac cacagcccac aagacagaag aagagaattc cgactcggac 540
 totgac 546

<210> 105

<211> 552

<212> DNA

<213> Homo sapiens

<400> 105

atggacggcc tgaggcagcg cgtggagcac ttcttggagc aaaggaacct ggtcacccgaa 60
 gtgctggggg cgctggaggc caagaccggg gtggagaagc ggtatctggc tgcaggagcc 120
 gtcactctgc taagcctgta totgctgttc ggctacggag cgtctctgct gtgcaatctc 180
 atcggatttg tgtaccccg c atatgcctca atcaaagcta tcgagagccc aagcaaggac 240
 gacgacaactg tgtggctcac ctactgggtg gtgtacgccc tgtttgggct ggccgagttc 300
 ttcagcgatc tactcctgtc ctggttccct ttctactacg tgggcaagtg cgccttctctg 360
 ttgtttctgca tggctcccag gccctggaac ggggctctca tgotgtatca gcgctgctg 420
 cgtccgctgt tcctaaggca ccacggggcc gtagacagaa tcatgaacga cctcagcggg 480
 cgagccctgg acgcggcggc cggaataacc aggaacgtca agccaagcca gaccccgag 540
 ccgaaggaca ag 552

<210> 106

<211> 420

<212> DNA

<213> Homo sapiens

<400> 106

atgagccgtt tcctgaatgt gttaagaagt tggctgggta tgggtgccat catagccatg 60
 gggaaacagc tgcagagctt ccgagaccac acttttctct atgaaaagct ctacactggc 120
 aagccaaacc ttgtgaatgg cctccaagct cggacctttg ggatctggac gctgctctca 180
 tcagtgtatc gctgcctctg tgccattgac attcacaaca agacgtctca tcacatcaca 240
 ctctggacct tcctccttgc cctggggcat ttctctctct agttgtttgt ctatggaact 300
 gcagctccca cgattggcgt cctggcacc ctgatggtgg caagtttctc catcctgggt 360

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atgctgggtcg ggctccggta tctagaagta gaaccagtat ccagacagaa gaagagaaac 420

<210> 107

<211> 459

<212> DNA

<213> Homo sapiens

<400> 107

atgaacgttg gagttgccca cagtgaagtg aatccaaata cccgtgtcat gaacagccgg 60
 ggtatgtggc tgacatatgc attgggagtt ggcttgcttc atattgtctt actcagcatt 120
 ccctttctca gtgttcctgt tgcttggact ttaacaaata ttatacataa tctggggatg 180
 tacgtatttt tgcattgcagt gaaaggaaca cctttogaaa ctctgacca gggtaaagca 240
 aggctcctaa ctcatggga acaactggac tatggagtac agtttacatc ttcacggaag 300
 tttttcaciaa tttctccaat aattctatat tttctggcaa gtttctatac gaagtatgat 360
 ccaactcact tcatcctaaa cacagcttct ctctgagtg tactaattcc caaatgccca 420
 caactacatg gtgttcggat ctttgaatt aataagtat 459

<210> 108

<211> 519

<212> DNA

<213> Homo sapiens

<400> 108

atggctgcct tcttgataca gaccaaggac aaccccatga aggccgtggg tgtgctggcc 60
 ggcaccatgg ccaccgtcgt ggccatcact gtcctcatct ccaccgccac cttctggcgc 120
 aacaagaagt ctaacaaggc cctgccaatg cggcgggtgc tccgcaagcg gccagccct 180
 gcgccccgca ccatccgcat tgagtggctc aagtccaaga gcaccaagc cgctaccaag 240
 ttcattgctca aagagaaacc tccaatgag aactgtaaca acaacagccc agaaagctct 300
 ctgctccgga gagctccggc tctccctcca ccaccagcg tggcgcccag cactggcgca 360
 gccagtgga ccgtgcctac tgtctctggc tctctcactc cgcagccgac ccaacccccg 420
 ccaaaaccca aaactatggg aagccccgtc cagtcaactc tgatctctga gctcaagcaa 480
 aagtttgaga agaagagtgt gcacaacaag gcttacttc 519

<210> 109

<211> 225

<212> DNA

<213> Homo sapiens

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<400> 109

atgatcggag acatcctgct gttegggacg ttgctgatga atgccggggc ggtgctgaac	60
tttaagctga aaaagaagga cacgcagggc tttggggagg agtccaggga gccagcaca	120
ggtgacaaca tccgggaatt cttgctgagc ctcagatact ttcgaaatct catcgccctg	180
tggaacatct tcatgatgtt ctgcattgatt gtgctgttcg gctct	225

<210> 110

<211> 477

<212> DNA

<213> Homo sapiens

<400> 110

atggagctgc ctgctgtgaa cctgaagggtg attctcctag gtcactggct gctgacaacc	60
tggggctgca ttgtattctc aggetcctat gcctgggcca acttcaccat cctggccttg	120
ggcgtgtggg ctgtggtcca gcgggactcc atcgacgcca taagcatgtt tctgggtggc	180
ttgctggcca ccatcttcct ggacatcgtg cacatcagca tctctaccc gcgggtcagc	240
ctcacggaca cgggcgcgtt tggcgtgggc atggccatcc tcagcttgct gctcaagccg	300
ctctcctgct gcttcgtcta ccacatgtac cgggagcgcg ggggtgagct cctggccacc	360
actggtttcc ttgggtcttc tcaggaccgt agtgccatcc agacgattga ctcagcagag	420
gcgcccgcag atccctttgc agtcccagag ggcaggagtc aagatgcccg aggggtac	477

<210> 111

<211> 3438

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (121)...(1032)

<400> 111

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cgggtacctg atggccacag agggctctag gaggccgagc gtgtaagcgg ggtgggcgcc	120
atg gag gca gag cag cgg ccg gcg gcg ggg gcc agc gaa ggg gcg acc	168
Met Glu Ala Glu Gln Arg Pro Ala Ala Gly Ala Ser Glu Gly Ala Thr	
1 5 10 15	
cct gga ctg gag gcg gtg cct ccc gtt gct ccc ccg cct gcg acc gcg	216
Pro Gly Leu Glu Ala Val Pro Pro Val Ala Pro Pro Pro Ala Thr Ala	

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20	25	30	
gcc tca ggt ccg atc ccc aaa tct ggg cct gag cct aag agg agg cac			264
Ala Ser Gly Pro Ile Pro Lys Ser Gly Pro Glu Pro Lys Arg Arg His			
35	40	45	
ctt ggg acg ctg ctc cag cct acg gtc aac aag ttc tcc ctt cgg gtg			312
Leu Gly Thr Leu Leu Gln Pro Thr Val Asn Lys Phe Ser Leu Arg Val			
50	55	60	
ttc ggc agc cac aaa gca gtg gaa atc gag cag gag cgg gtg aag tca			360
Phe Gly Ser His Lys Ala Val Glu Ile Glu Gln Glu Arg Val Lys Ser			
65	70	75	80
gcg ggg gcc tgg atc atc cac ccc tac agc gac ttc cgg ttt tac tgg			408
Ala Gly Ala Trp Ile Ile His Pro Tyr Ser Asp Phe Arg Phe Tyr Trp			
85	90	95	
gac ctg atc atg ctg ctg ctg atg gtg ggg aac ctc atc gtc ctg cct			456
Asp Leu Ile Met Leu Leu Leu Met Val Gly Asn Leu Ile Val Leu Pro			
100	105	110	
gtg ggc atc acc ttc ttc aag gag gag aac tcc ccg cct tgg atc gtc			504
Val Gly Ile Thr Phe Phe Lys Glu Glu Asn Ser Pro Pro Trp Ile Val			
115	120	125	
ttc aac gta ttg tct gat act ttc ttc cta ctg gat ctg gtg ctc aac			552
Phe Asn Val Leu Ser Asp Thr Phe Phe Leu Leu Asp Leu Val Leu Asn			
130	135	140	
ttc cga acg ggc atc gtg gtg gag gag ggt gct gag atc ctg ctg gca			600
Phe Arg Thr Gly Ile Val Val Glu Glu Gly Ala Glu Ile Leu Leu Ala			
145	150	155	160
ccg cgg gcc atc cgc acg cgc tac ctg cgc acc tgg ttc ctg gtt gac			648
Pro Arg Ala Ile Arg Thr Arg Tyr Leu Arg Thr Trp Phe Leu Val Asp			
165	170	175	
ctc atc tct tct atc cct gtg gat tac atc ttc cta gtg gtg gag ctg			696
Leu Ile Ser Ser Ile Pro Val Asp Tyr Ile Phe Leu Val Val Glu Leu			
180	185	190	
gag cca cgg ttg gac gct gag gtc tac aaa acg gca cgg gcc cta cgc			744
Glu Pro Arg Leu Asp Ala Glu Val Tyr Lys Thr Ala Arg Ala Leu Arg			
195	200	205	
atc gtt cgc ttc acc aag atc cta agc ctg ctg agg ctg ctc cgc ctc			792

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Ile Val Arg Phe Thr Lys Ile Leu Ser Leu Leu Arg Leu Leu Arg Leu
 210 215 220
 tcc cgc ctc atc cgc tac ata cac cag tgg gag gag atc ttt cac atg 840
 Ser Arg Leu Ile Arg Tyr Ile His Gln Trp Glu Glu Ile Phe His Met
 225 230 235 240
 acc tat gac ctg gcc agt gct gtg gtt cgc atc ttc aac ctc att ggg 888
 Thr Tyr Asp Leu Ala Ser Ala Val Val Arg Ile Phe Asn Leu Ile Gly
 245 250 255
 atg atg ctg ctg cta tgt cac tgg gat ggc tgt ctg cag ttc ctg gtg 936
 Met Met Leu Leu Leu Cys His Trp Asp Gly Cys Leu Gln Phe Leu Val
 260 265 270
 ccc atg ctg cag gac ttc cct ccc gac tgc tgg gtc tcc atc aac cac 984
 Pro Met Leu Gln Asp Phe Pro Pro Asp Cys Trp Val Ser Ile Asn His
 275 280 285
 atg gtg gtg aga agt ccc cac agc tct gcc ttt cct ggg cct tct t 1030
 Met Val Val Arg Ser Pro His Ser Ser Ala Phe Pro Gly Pro Ser
 290 295 300
 agggctcttc tgccctgagta gcagggatgg ccacagggag caggaggtgg gagatgatca 1090
 caacagaaaa taggagcagag gaggtgggga ggagggagga aaggggaagg agaccagaa 1150
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 tactttgggg agatctgcct gctaactagg gcccggcgca cagccagtgt tcgggctgac 2050
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cccatgatgc gccgggcctt tgagactgtg gccatggatc ggctgctccg catcggcaag 2170
aagaattcca tactgcagcg gaagcgctcc gagccaagtc caggcagcag tgggtggcatc 2230
atggagcagc acttggtgca acatgacaga gacatggctc ggggtgttcg gggtcggggc 2290
ccgagcacag gagctcagct tagtggaaaag ccagtactgt gggagccact ggtacatgcg 2350
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tatgtacca agggcagatg cctcttgggg aaggccatgg ggacctgaaa cattgcccc 2950
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ttgttttgtt ttttcctct gagtttctg ttggtgcagg aataaggga aggcccaagg 3310
tatccaagcc tggggaaggg caggccagcc agcacctctg ccttctcagg gacaagagta 3370
gtcctttacc acctcactc tgctgtccc ctctcctact ctacagcatt aaagactgtg 3420
ggaccagg 3438

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<210> 112

<211> 1144

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (56)...(907)

<400> 112

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atg gcc gac ccc cac cag ctt ttc gat gac aca agt tca gcc cag agc 103
Met Ala Asp Pro His Gln Leu Phe Asp Asp Thr Ser Ser Ala Gln Ser

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1	5	10	15	
cgg ggc tat ggg gcc cag cgg gca cct ggt ggc ctg agt tat cct gca				151
Arg Gly Tyr Gly Ala Gln Arg Ala Pro Gly Gly Leu Ser Tyr Pro Ala				
20	25	30		
gcc tct ccc acg ccc cat gca gcc ttc ctg gct gac ccg gtg tcc aac				199
Ala Ser Pro Thr Pro His Ala Ala Phe Leu Ala Asp Pro Val Ser Asn				
35	40	45		
atg gcc atg gcc tat ggg agc agc ctg gcc gcg cag ggc aag gag ctg				247
Met Ala Met Ala Tyr Gly Ser Ser Leu Ala Ala Gln Gly Lys Glu Leu				
50	55	60		
gtg gat aag aac atc gac cgc ttc atc ccc atc acc aag ctc aag tat				295
Val Asp Lys Asn Ile Asp Arg Phe Ile Pro Ile Thr Lys Leu Lys Tyr				
65	70	75	80	
tac ttt gct gtg gac acc atg tat gtg ggc aga aag ctg ggc ctg ctg				343
Tyr Phe Ala Val Asp Thr Met Tyr Val Gly Arg Lys Leu Gly Leu Leu				
85	90	95		
ttc ttc ccc tac cta cac cag gac tgg gaa gtg cag tac caa cag gac				391
Phe Phe Pro Tyr Leu His Gln Asp Trp Glu Val Gln Tyr Gln Gln Asp				
100	105	110		
acc ccg gtg gcc ccc cgc ttt gac gtc aat gcc ccg gac ctc tac att				439
Thr Pro Val Ala Pro Arg Phe Asp Val Asn Ala Pro Asp Leu Tyr Ile				
115	120	125		
cca gca atg gct ttc atc acc tac gtt ttg gtg gct ggt ctt gcg ctg				487
Pro Ala Met Ala Phe Ile Thr Tyr Val Leu Val Ala Gly Leu Ala Leu				
130	135	140		
ggg acc cag gat agg ttc tcc cca gac ctc ctg ggg ctg caa gcg agc				535
Gly Thr Gln Asp Arg Phe Ser Pro Asp Leu Leu Gly Leu Gln Ala Ser				
145	150	155	160	
tca gcc ctg gcc tgg ctg acc ctg gag gtg ctg gcc atc ctg ctc agc				583
Ser Ala Leu Ala Trp Leu Thr Leu Glu Val Leu Ala Ile Leu Leu Ser				
165	170	175		
ctc tat ctg gtc act gtc aac acc gac ctc acc acc atc gac ctg gtg				631
Leu Tyr Leu Val Thr Val Asn Thr Asp Leu Thr Thr Ile Asp Leu Val				
180	185	190		
gcc ttc ttg ggc tac aaa tat gtc ggg atg att ggc ggg gtc ctc atg				679

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Ala Phe Leu Gly Tyr Lys Tyr Val Gly Met Ile Gly Gly Val Leu Met
 195 200 205
 ggc ctg ctc ttc ggg aag att ggc tac tac ctg gtg ctg ggc tgg tgc 727
 Gly Leu Leu Phe Gly Lys Ile Gly Tyr Tyr Leu Val Leu Gly Trp Cys
 210 215 220
 tgc gta gcc atc ttt gtg ttc atg atc cgg acg ctg cgg ctg aag atc 775
 Cys Val Ala Ile Phe Val Phe Met Ile Arg Thr Leu Arg Leu Lys Ile
 225 230 235 240
 ttg gca gac gca gca gct gag ggg gtc cgg gtg cgt ggg gcc cgg aac 823
 Leu Ala Asp Ala Ala Ala Glu Gly Val Pro Val Arg Gly Ala Arg Asn
 245 250 255
 cag ctg cgc atg tac ctg acc atg gcg gtg gcg gcg gcg cag cct atg 871
 Gln Leu Arg Met Tyr Leu Thr Met Ala Val Ala Ala Ala Gln Pro Met
 260 265 270
 ctc atg tac tgg ctc acc ttc cac ctg gtg cgg tgagcgcgcc cgtga 920
 Leu Met Tyr Trp Leu Thr Phe His Leu Val Arg
 275 280
 acctcccgt gctgctgctg ctgctggggg ccaactgtggc cgccgaactc atctcctgcc 980
 tgcaggcccc aaggtccacc ctgtctggcc acaggcaccg cctccatccc atgtcccgcc 1040
 cagccccgcc cccaacccaa ggtgctgaga gatctccagc tgcacaggcc accgccccag 1100
 ggcgtggcgc ctgttacaga aacaataaac cctgatgggc atgg 1144

 <210> 113
 <211> 2339
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (253)...(1719)
 <400> 113
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 tagatttggg caaggacttt agattcgggc totgttctgt ttccgcgcgc ctgottcctg 120
 ccgaggctgg ccagggcagc cgcgcttcga aggacgccgc cgggagctgc ggagcatgcg 180
 tggagtggca gtgctaaccg ctggtgtctc gcaactgttg cctgtgaagg tacgtgaagc 240
 tgaagacctg ga atg gct gga aag ggg tca tca ggc agg cgg ccc ctg 288

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Met Ala Gly Lys Gly Ser Ser Gly Arg Arg Pro Leu																			
1						5						10							
ctg	ctg	ggg	ctg	ctg	gtg	gcc	gta	gcc	act	gtc	cac	ctg	gtc	atc	tgt		336		
Leu	Leu	Gly	Leu	Leu	Val	Ala	Val	Ala	Thr	Val	His	Leu	Val	Ile	Cys				
15						20						25							
ccc	tac	acc	aaa	gtg	gag	gag	agc	ttc	aac	ctg	cag	gcc	aca	cat	gac		384		
Pro	Tyr	Thr	Lys	Val	Glu	Glu	Ser	Phe	Asn	Leu	Gln	Ala	Thr	His	Asp				
30						35						40							
ctg	ctc	tac	cac	tgg	caa	gac	ctg	gag	cag	tac	gac	cat	ctt	gag	ttc		432		
Leu	Leu	Tyr	His	Trp	Gln	Asp	Leu	Glu	Gln	Tyr	Asp	His	Leu	Glu	Phe				
45						50						55						60	
ccc	gga	gtc	gtc	ccc	agg	acg	ttc	ctc	ggg	cca	gtg	gtg	atc	gca	gtg		480		
Pro	Gly	Val	Val	Pro	Arg	Thr	Phe	Leu	Gly	Pro	Val	Val	Ile	Ala	Val				
65						70						75							
ttc	tcc	agc	ccc	gcg	gtt	tac	gtg	ctt	tcg	ctg	tta	gaa	atg	tcc	aag		528		
Phe	Ser	Ser	Pro	Ala	Val	Tyr	Val	Leu	Ser	Leu	Leu	Glu	Met	Ser	Lys				
80						85						90							
ttt	tac	tct	cag	cta	ata	gtt	aga	gga	gtg	ctt	gga	ctc	ggc	gtg	att		576		
Phe	Tyr	Ser	Gln	Leu	Ile	Val	Arg	Gly	Val	Leu	Gly	Leu	Gly	Val	Ile				
95						100						105							
ttt	gga	ctc	tgg	acg	tta	caa	aag	gaa	gtg	aga	cgg	cac	ttc	ggg	gcc		624		
Phe	Gly	Leu	Trp	Thr	Leu	Gln	Lys	Glu	Val	Arg	Arg	His	Phe	Gly	Ala				
110						115						120							
atg	gtg	gcc	acc	atg	ttc	tgc	tgg	gtg	acg	gcc	atg	cag	ttc	cac	ctg		672		
Met	Val	Ala	Thr	Met	Phe	Cys	Trp	Val	Thr	Ala	Met	Gln	Phe	His	Leu				
125						130						135						140	
atg	ttc	tac	tgc	acg	cgg	aca	ctg	ccc	aat	gtg	ctg	gcc	ctg	cct	gta		720		
Met	Phe	Tyr	Cys	Thr	Arg	Thr	Leu	Pro	Asn	Val	Leu	Ala	Leu	Pro	Val				
145						150						155							
gtc	ctg	ctg	gcc	ctc	gcg	gcc	tgg	ctg	cgg	cac	gag	tgg	gcc	cgc	ttc		768		
Val	Leu	Leu	Ala	Leu	Ala	Ala	Trp	Leu	Arg	His	Glu	Trp	Ala	Arg	Phe				
160						165						170							
atc	tgg	ctg	tca	gcc	ttc	gcc	atc	atc	gtg	ttc	agg	gtg	gag	ctg	tgc		816		
Ile	Trp	Leu	Ser	Ala	Phe	Ala	Ile	Ile	Val	Phe	Arg	Val	Glu	Leu	Cys				
175						180						185							

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ctg ttc ctg ggc ctc ctg ctg ctg ctg gcc ttg ggc aac cga aag gtt	864
Leu Phe Leu Gly Leu Leu Leu Leu Leu Ala Leu Gly Asn Arg Lys Val	
190 195 200	
tct gta gtc aga gcc ctt cgc cac gcc gtc ccg gca ggg atc ctc tgt	912
Ser Val Val Arg Ala Leu Arg His Ala Val Pro Ala Gly Ile Leu Cys	
205 210 215 220	
tta gga ctg acg gtt gct gtg gac tct tat ttt tgg cgg cag ctc act	960
Leu Gly Leu Thr Val Ala Val Asp Ser Tyr Phe Trp Arg Gln Leu Thr	
225 230 235	
tgg ccg gaa gga aag gtg ctt tgg tac aac act gtc ctg aac aaa agc	1008
Trp Pro Glu Gly Lys Val Leu Trp Tyr Asn Thr Val Leu Asn Lys Ser	
240 245 250	
tcc aac tgg ggg acc tcc ccg ctg ctg tgg tac ttc tac tca gcc ctg	1056
Ser Asn Trp Gly Thr Ser Pro Leu Leu Trp Tyr Phe Tyr Ser Ala Leu	
255 260 265	
ccc cgc ggc ctg ggc tgc agc ctg ctc ttc atc ccc ctg ggc ttg gta	1104
Pro Arg Gly Leu Gly Cys Ser Leu Leu Phe Ile Pro Leu Gly Leu Val	
270 275 280	
gac aga agg acg cac gcg ccg acg gtg ctg gca ctg ggc ttc atg gca	1152
Asp Arg Arg Thr His Ala Pro Thr Val Leu Ala Leu Gly Phe Met Ala	
285 290 295 300	
ctc tac tcc ctc ctg cca cac aag gag cta cgc ttc atc atc tat gcc	1200
Leu Tyr Ser Leu Leu Pro His Lys Glu Leu Arg Phe Ile Ile Tyr Ala	
305 310 315	
ttc ccc atg ctc aac atc acg gct gcc aga ggc tgc tcc tac ctg ctg	1248
Phe Pro Met Leu Asn Ile Thr Ala Ala Arg Gly Cys Ser Tyr Leu Leu	
320 325 330	
aat aac tat aaa aag tct tgg ctg tac aaa gca ggg tct ctg ctt gtg	1296
Asn Asn Tyr Lys Lys Ser Trp Leu Tyr Lys Ala Gly Ser Leu Leu Val	
335 340 345	
atc gga cac ctc gtg gtg aat gcc gcc tac tca gcc acg gcc ctg tat	1344
Ile Gly His Leu Val Val Asn Ala Ala Tyr Ser Ala Thr Ala Leu Tyr	
350 355 360	
gtg tcc cat ttc aac tac cca ggt ggc gtc gca atg cag agg ctg cac	1392
Val Ser His Phe Asn Tyr Pro Gly Gly Val Ala Met Gln Arg Leu His	

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365	370	375	380	
cag ctg gtg ccc ccc cag aca gac gtc ctt ctg cac att gac gtg gca				1440
Gln Leu Val Pro Pro Gln Thr Asp Val Leu Leu His Ile Asp Val Ala				
385	390	395		
gcc gcc cag aca ggt gtg tct cgg ttt ctc caa gtc aac agc gcc tgg				1488
Ala Ala Gln Thr Gly Val Ser Arg Phe Leu Gln Val Asn Ser Ala Trp				
400	405	410		
agg tac gac aag agg gag gat gtg cag ccg ggg aca ggc atg ctg gca				1536
Arg Tyr Asp Lys Arg Glu Asp Val Gln Pro Gly Thr Gly Met Leu Ala				
415	420	425		
tac aca cac atc ctc atg gag gcg gcc cct ggg ctc ctg gcc ctc tac				1584
Tyr Thr His Ile Leu Met Glu Ala Ala Pro Gly Leu Leu Ala Leu Tyr				
430	435	440		
agg gac aca cac cgg gtc ctg gcc agc gtc gtg ggg acc aca ggt gtg				1632
Arg Asp Thr His Arg Val Leu Ala Ser Val Val Gly Thr Thr Gly Val				
445	450	455	460	
agt ctg aac ctg acc caa ctg ccc ccc ttc aac gtc cac ctg cag aca				1680
Ser Leu Asn Leu Thr Gln Leu Pro Pro Phe Asn Val His Leu Gln Thr				
465	470	475		
aag ctg gtg ctt ctg gag agg ctc ccc cgg ccg tcc tgagggggac cagg				1730
Lys Leu Val Leu Leu Glu Arg Leu Pro Arg Pro Ser				
480	485			
cagccctcag cagccacagg ccttcacagga gctgttatca ctaccagttt ctggcacaat				1790
tccagcaciaa ttatgacaat tcagagaagc aagtcaaagg actgggcacc tgcctctgac				1850
agacaccaga ccaggtccag ggccctcctcc acagcctcag ctggggctct cagcaccaaa				1910
gaacgagggg cccaggtctt gttggcacc cgggagccac tgcccagggt gatggtggcc				1970
agctcagggc ttcctgcggg tgactgtcgc ccagaccagg tgccattcat gactaatcag				2030
gagcagcggg ctcacccagg cacctgtctg ccaggaggcc acgtgtgtcc tgcccaccca				2090
gggggagctg tattttggca gcacccacg cttgtctgcc gagggcctct tggggcacct				2150
aagacagcac cccctctcag gggagaccat ggtggccccg gccgcacccc cccaccctgg				2210
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gaacctctc				2339

178/233

<211> 1756

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (102)...(650)

<400> 114

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                                     Met Trp Pro Pro
                                     1
gac ccc gac ccc gac ccg gac ccc gag cct gcc ggc ggc tcc cgt ccc      161
Asp Pro Asp Pro Asp Pro Asp Pro Glu Pro Ala Gly Gly Ser Arg Pro
   5              10              15              20
ggc ccc gcg gtc ccc ggg ctc cgc gcc ctg ctg ccg gcg cgg gct ttc      209
Gly Pro Ala Val Pro Gly Leu Arg Ala Leu Leu Pro Ala Arg Ala Phe
              25              30              35
ctc tgc tct ctc aaa ggc cgc ctc ctg ctg gcc gag tgg ggt ctc tca      257
Leu Cys Ser Leu Lys Gly Arg Leu Leu Leu Ala Glu Ser Gly Leu Ser
              40              45              50
ttc atc act ttt atc tgc tat gtg gcg tcc tca gca tct gcc ttc ctc      305
Phe Ile Thr Phe Ile Cys Tyr Val Ala Ser Ser Ala Ser Ala Phe Leu
              55              60              65
aca gcg cct ctg ctg gag ttc ctg ctg gcc ttg tac ttc ctc ttt gct      353
Thr Ala Pro Leu Leu Glu Phe Leu Leu Ala Leu Tyr Phe Leu Phe Ala
              70              75              80
gat gcc atg cag ctg aat gac aag tgg cag ggc ttg tgc tgg ccc atg      401
Asp Ala Met Gln Leu Asn Asp Lys Trp Gln Gly Leu Cys Trp Pro Met
              85              90              95              100
atg gac ttc ctg cgc tgt gtc acc gcg gcc ctc atc tac ttt gct atc      449
Met Asp Phe Leu Arg Cys Val Thr Ala Ala Leu Ile Tyr Phe Ala Ile
              105              110              115
tcc atc acg gcc atc gcc aag tac tgg gat ggg gct tcc aaa gcc gct      497
Ser Ile Thr Ala Ile Ala Lys Tyr Ser Asp Gly Ala Ser Lys Ala Ala
              120              125              130

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ggg gtg ttt ggc ttc ttt gct acc atc gtg ttt gca act gat ttc tac 545
 Gly Val Phe Gly Phe Phe Ala Thr Ile Val Phe Ala Thr Asp Phe Tyr
 135 140 145
 ctg atc ttt aac gac gtg gcc aaa ttc ctc aaa caa ggg gac tct gca 593
 Leu Ile Phe Asn Asp Val Ala Lys Phe Leu Lys Gln Gly Asp Ser Ala
 150 155 160
 gat gag acc aca gcc cac aag aca gaa gaa gag aat tcc gac tcg gac 641
 Asp Glu Thr Thr Ala His Lys Thr Glu Glu Glu Asn Ser Asp Ser Asp
 165 170 175 180
 tct gac tgaaggcctg gcgggtgcct tggcaacctg agccacacag gcc 690
 Ser Asp

tccaccctctg cgctcacag gggctcgtgg cgttgagcgg gaggcctgga cttctgagtt 750
 gcagaggggg ctgcggacac agcaggcccc ctacagcctc aggttctgcc tgagcccagc 810
 ctaccaggct tgccctcag ctacagactg ttgaccacgc tgcgtatgag ggcattcttg 870
 gtatcccaact cttctcccc atttctgtcc cacaggcctt cagcccttta acgtctctgc 930
 caaaaaccag cacaaggaga caaagcagag ccttgtctgt atctgggcag caggtgttcc 990
 atgctgctag gtggcggggg tcgggggtct tctgtttcac taacaggaa aaagacagaa 1050
 acctgacag ggctgccccg ccaggccccg gtgggtttgt ctgcaacttg tgctcctgcc 1110
 cacaccagcc actttggtga caatgacct tccaagaatc tttggttcaa ggagcaccag 1170
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 ggctcggcac ccataactaa cacctcccac ccttggaac catgtctctt gggggtgaga 1290
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 tattttttta tgcaaaagca gcttcttaac agatggcatt ttctgtgact ctaggcctca 1650
 caaaagagcc agagttctgg acctatgttt ggagcatttg tagccttatt ctcttgctg 1710
 tgaatctctt acctgaaaa aaagccataa tgaattaagc caaaag 1756

<210> 115

<211> 1418

<212> DNA

<213> Homo sapiens

180/233

<220>

<221> CDS

<222> (149)...(703)

<400> 115

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ggctgcggga aagcgggtgcg cgtgcagcgg ggtgggtgcc ctggtccgcg ggcgagctcg      120
agcagccaac cccgggcgcg tcggggcc atg gac ggc ctg agg cag cgc gtg      172
                                Met Asp Gly Leu Arg Gln Arg Val
                                1           5
gag cac ttc ctg gag caa agg aac ctg gtc acc gaa gtg ctg ggg gcg      220
Glu His Phe Leu Glu Gln Arg Asn Leu Val Thr Glu Val Leu Gly Ala
    10           15           20
ctg gag gcc aag acc ggg gtg gag aag cgg tat ctg gct gca gga gcc      268
Leu Glu Ala Lys Thr Gly Val Glu Lys Arg Tyr Leu Ala Ala Gly Ala
    25           30           35           40
gtc act ctg cta agc ctg tat ctg ctg ttc ggc tac gga gcg tct ctg      316
Val Thr Leu Leu Ser Leu Tyr Leu Leu Phe Gly Tyr Gly Ala Ser Leu
            45           50           55
otg tgc aat ctc atc gga ttt gtg tac ccc gca tat gcc tca atc aaa      364
Leu Cys Asn Leu Ile Gly Phe Val Tyr Pro Ala Tyr Ala Ser Ile Lys
            60           65           70
gct atc gag agc cca agc aag gac gac gac act gtg tgg ctc acc tac      412
Ala Ile Glu Ser Pro Ser Lys Asp Asp Asp Thr Val Trp Leu Thr Tyr
            75           80           85
tgg gtg gtg tac gcc ctg ttt ggg ctg gcc gag ttc ttc agc gat cta      460
Trp Val Val Tyr Ala Leu Phe Gly Leu Ala Glu Phe Phe Ser Asp Leu
            90           95           100
ctc ctg tcc tgg ttc cct ttc tac tac gtg ggc aag tgc gcc ttc ctg      508
Leu Leu Ser Trp Phe Pro Phe Tyr Tyr Val Gly Lys Cys Ala Phe Leu
    105           110           115           120
ttg ttc tgc atg gct ccc agg ccc tgg aac ggg gct ctc atg ctg tat      556
Leu Phe Cys Met Ala Pro Arg Pro Trp Asn Gly Ala Leu Met Leu Tyr
            125           130           135
cag cgc gtc gtg cgt ccg ctg ttc cta agg cac cac ggg gcc gta gac      604
Gln Arg Val Val Arg Pro Leu Phe Leu Arg His His Gly Ala Val Asp

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140	145	150	
aga atc atg aac gac ctc agc ggg cga gcc ctg gac gcg gcc gga			652
Arg Ile Met Asn Asp Leu Ser Gly Arg Ala Leu Asp Ala Ala Gly			
155	160	165	
ata acc agg aac gtc aag cca agc cag acc ccg cag ccg aag gac aag			700
Ile Thr Arg Asn Val Lys Pro Ser Gln Thr Pro Gln Pro Lys Asp Lys			
170	175	180	
tgaagcagcc cctgagcct cacaaggacc tcctggetgg tgaggagggg gccgcgccag			760
gctcccaggc ctccacagag tottcagcgc atcccccaac agcagcccct gccagtcctt			820
cgggtccagg caaggccctg ggggtctcct taaatgccac ctcgggcaag tcccagtcct			880
agtctctggc cccccccagc totggatccc agggccagct gccctctggc tctggetgtg			940
gctccgcct gtccggcagg gcccagggcc agcgtcgggc acagggcagc tcccactggt			1000
ctcggaaca caccagccg cctggtactt cctccggccc ctcccagtcg gccctcccgt			1060
cctcggggccc cctgcagcca cccaacgtca cctccagccc ggtctcacc atggtccagt			1120
ctcccagcag cagcaacatc cccacgcagc cccccagcaa gtctctggc aagccggagg			1180
acgcagcccc caagaccagc ggacagcgcc agaaggaatc gtcgaaacag cctgccagca			1240
gogctcagc gcccgagctg gtccctgccc attccgggac ctctctggag tacacttcgg			1300
agtccaccac cgagatcacc tgcagctggc cacaccacag gccccctgc ctgcagcact			1360
actggtgctt gaaacacctg gcctgctagg aggtccaat aaagctaacc cggaccag			1418

<210> 116

<211> 1211

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (133)...(555)

<400> 116

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ggctgctgct gccactgctg tgcggggggc ccggtcgcca ggcaaaaagc cctcccacgt	120
ttgaggggag tc atg agc cgt ttc ctg aat gtg tta aga agt tgg ctg	168

Met Ser Arg Phe Leu Asn Val Leu Arg Ser Trp Leu

1

5

10

ggt atg gtg tcc atc ata gcc atg ggg aac acg ctg cag agc ttc cga	216
Val Met Val Ser Ile Ile Ala Met Gly Asn Thr Leu Gln Ser Phe Arg	

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15	20	25	
gac cac act ttt ctc tat gaa aag ctc tac act ggc aag cca aac ctt			264
Asp His Thr Phe Leu Tyr Glu Lys Leu Tyr Thr Gly Lys Pro Asn Leu			
30	35	40	
gtg aat ggc ctc caa gct cgg acc ttt ggg atc tgg acg ctg ctc tca			312
Val Asn Gly Leu Gln Ala Arg Thr Phe Gly Ile Trp Thr Leu Leu Ser			
45	50	55	60
tca gtg att cgc tgc ctc tgt gcc att gac att cac aac aag acg ctc			360
Ser Val Ile Arg Cys Leu Cys Ala Ile Asp Ile His Asn Lys Thr Leu			
65	70	75	
tat cac atc aca ctc tgg acc ttc ctc ctt gcc ctg ggg cat ttc ctc			408
Tyr His Ile Thr Leu Trp Thr Phe Leu Leu Ala Leu Gly His Phe Leu			
80	85	90	
tct gag ttg ttt gtc tat gga act gca got ccc acg att ggc gtc ctg			456
Ser Glu Leu Phe Val Tyr Gly Thr Ala Ala Pro Thr Ile Gly Val Leu			
95	100	105	
gca ccc ctg atg gtg gca agt ttc tcc atc ctg ggt atg ctg gtc ggg			504
Ala Pro Leu Met Val Ala Ser Phe Ser Ile Leu Gly Met Leu Val Gly			
110	115	120	
ctc cgg tat cta gaa gta gaa cca gta tcc aga cag aag aag aga aac			552
Leu Arg Tyr Leu Glu Val Glu Pro Val Ser Arg Gln Lys Lys Arg Asn			
125	130	135	140
tgaggcca gcattatcac ctccaggact ttctcgtttt ccaccttggc catcttcttc			610
cttcgtcgtc tctcctcttt aatttctttt ctattccatc atctgccctt ttattcaact			670
ttagcctctt tttttaattt ttaaaattta aagatatgca tactgaaaag tatataacat			730
gtacgtacaa tttaaagaat aattttaaag tgaatactac gtaactccat ccaagtcaag			790
aaattgccag cttctcggaa gccactgtg tctccttccc ctacctgcaa cctcttcag			850
gctccctttt ccagccttcc cctttttccc ttttattttc atgccttgat ttgacttggt			910
tggtgggaac atgtgaacta tgaaacttaa acctgctgcc caccagagc agctgtgacc			970
aagggtgcc tcaaggggtt gtccacgcag gttgggctcc tctctgctgc tggaccaag			1030
actctgaacc ttccaaggga caggcagttc ttctaagaag ggctcccctg tgtgtgagca			1090
agaccacagc tctccttcta tctacagatg catgagggtt ggaagagtct gggctgtttt			1150
tagaccttct ggtcagctgt atttgtgtaa caacttttgt aataaataga aaaaccctct			1210
g			1211

183/233

<210> 117

<211> 1099

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (183)...(644)

<400> 117

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ggcggcatgt accttcacac ttgagtattc agaaagaagt gatctgaact ctgaccattc      120
tttatggata cattaagtca aatataagag tctgactact tgacacactg gctcgagcaa      180
ac atg aac gtt gga gtt gcc cac agt gaa gtg aat cca aat acc cgt      227
Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg
      1           5           10          15
gtc atg aac agc cgg ggt atg tgg ctg aca tat gca ttg gga gtt ggc      275
Val Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly
      20          25          30
ttg ctt cat att gtc tta ctc agc att ccc ttc ttc agt gtt cct gtt      323
Leu Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val
      35          40          45
gct tgg act tta aca aat att ata cat aat ctg ggg atg tac gta ttt      371
Ala Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe
      50          55          60
ttg cat gca gtg aaa gga aca cct ttc gaa act cct gac cag ggt aaa      419
Leu His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys
      65          70          75
gca agg ctc cta act cat tgg gaa caa ctg gac tat gga gta cag ttt      467
Ala Arg Leu Leu Thr His Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe
      80          85          90          95
aca tct tca cgg aag ttt ttc aca att tct cca ata att cta tat ttt      515
Thr Ser Ser Arg Lys Phe Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe
      100         105         110
ctg gca agt ttc tat acg aag tat gat cca act cac ttc atc cta aac      563
Leu Ala Ser Phe Tyr Thr Lys Tyr Asp Pro Thr His Phe Ile Leu Asn
      115         120         125

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aca gct tct ctc ctg agt gta cta att ccc aaa atg cca caa cta cat 611
 Thr Ala Ser Leu Leu Ser Val Leu Ile Pro Lys Met Pro Gln Leu His
 130 135 140
 ggt gtt cgg atc ttt gga att aat aag tat tgaaatgttt tgaaactga 660
 Gly Val Arg Ile Phe Gly Ile Asn Lys Tyr
 145 150
 aaaaaaattt tacagctact gaattttotta taaggaagga gtgggttagta aactgcactg 720
 tttctctgat aatgtgaaat gagaagtatt tacattggag ggccaatggc tggctcettca 780
 agtgctgttt tgaagtgcag atttccatta aatgatgcct ctgtttaata cacctggtac 840
 atttctgaag aggggcttta taagcaggct gggcaggccc agcttataag ttaaagggca 900
 tcacagttag ggtgtagtag ataaattcaa ggaaataaga gatttgtaag aaactaggac 960
 cagcttaact tataatgaat gggcattgtg ttaagaaaag aacatttcca gtcattcagc 1020
 tgtggttatt taaagcagac ttacatgtaa accggaatcc tctctataca agtttattaa 1080
 agattatttt tattaccgt 1099

<210> 118

<211> 3489

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (227)...(748)

<400> 118

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 aaaagcccat agtgcctatc agattctcaa agggactcct gaetccagaa agtttaaaaa 120
 ccattaggct taaggaagca catacctact ctgtactcca gggaccaggt gggaaacagct 180
 gagtgcaggg agtggttttc totttcagac cctctcccgg agcccc atg gct gcc 235
 Met Ala Ala
 1
 ttc ctg ata cag acc aag gac aac ccc atg aag gcc gtg ggt gtg ctg 283
 Phe Leu Ile Gln Thr Lys Asp Asn Pro Met Lys Ala Val Gly Val Leu
 5 10 15
 gcc ggc acc atg gcc acc gtc gtg gcc atc act gtc ctc atc tcc acc 331
 Ala Gly Thr Met Ala Thr Val Val Ala Ile Thr Val Leu Ile Ser Thr
 20 25 30 35

185/233

gcc acc ttc tgg cgc aac aag aag tct aac aag gtc ctg cca atg cgg 379
 Ala Thr Phe Trp Arg Asn Lys Lys Ser Asn Lys Val Leu Pro Met Arg
 40 45 50
 cgg gtg ctc cgc aag cgg ccc agc cct gcg ccc cgc acc atc cgc att 427
 Arg Val Leu Arg Lys Arg Pro Ser Pro Ala Pro Arg Thr Ile Arg Ile
 55 60 65
 gag tgg ctc aag tcc aag agc acc aaa gcc gct acc aag ttc atg ctc 475
 Glu Trp Leu Lys Ser Lys Ser Thr Lys Ala Ala Thr Lys Phe Met Leu
 70 75 80
 aaa gag aaa cct ccc aat gag aac tgt aac aac aac agc cca gaa agc 523
 Lys Glu Lys Pro Pro Asn Glu Asn Cys Asn Asn Asn Ser Pro Glu Ser
 85 90 95
 tct ctg ctc ccg aga gct ccg gct ctc cct cca cca ccc agc gtg gcg 571
 Ser Leu Leu Pro Arg Ala Pro Ala Leu Pro Pro Pro Pro Ser Val Ala
 100 105 110 115
 ccc agc act ggc gca gcc cag tgg acc gtg cct act gtc tct ggc tct 619
 Pro Ser Thr Gly Ala Ala Gln Trp Thr Val Pro Thr Val Ser Gly Ser
 120 125 130
 ctc act ccg cag ccg acc caa ccc ccg cca aaa ccc aaa act atg gga 667
 Leu Thr Pro Gln Pro Thr Gln Pro Pro Pro Lys Pro Lys Thr Met Gly
 135 140 145
 agc ccc gtc cag tca act ctg atc tct gag ctc aag caa aag ttt gag 715
 Ser Pro Val Gln Ser Thr Leu Ile Ser Glu Leu Lys Gln Lys Phe Glu
 150 155 160
 aag aag agt gtg cac aac aag gct tac ttc tagtgtatgc cctat 760
 Lys Lys Ser Val His Asn Lys Ala Tyr Phe
 165 170
 gaccccccat ctttctccg ccctgaccc ccaccacct gctgctcgga ctatgtcccc 820
 cttcctctgc tccttaaggt cactgacccc tgttttgcac aatggtataa tccccactgt 880
 cctcatctct accgccacct tctggcgcaa caagaagttg cgctctgaca gggctctagt 940
 cagggccttg ggcaagacat tgggctctag gatgcaattg gcaaatacgt ccccgttact 1000
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 cagctcacc atcccagacc tcacagtcctc tcaggtteta ctgggatctc atcatcatcc 1120
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 cgcctgcagc tgagagcagg agcaggaaaa ggaggctcag cactgtctca ggctggaggt 1240

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cagcgaacct	cgtgggctgt	aggaaagcaa	atgtaggtaa	ggggagagca	aggatgcaca	1300
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cagggctgag	atgtggtgag	acttccgttt	ttatccagct	cttttgccta	catcgcgtaa	1660
ccttgggaaa	gctgtttaaa	gtcgtgtatc	atcctcttcc	tcactctgaa	atgaagaaag	1720
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gcaggcaactg	tgttgggtct	aggggtctac	actggatgat	ggcattgccg	tgactcacac	1960
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gcacagagag	agaaaagtag	aacagttctt	tgcatttggc	tctacttact	aacaacccct	2320
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taaatggaaa	ataaagtctg	ttacccaaag	gccatgctga	tccctgtctc	cctgtcttca	2680
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gccatggatg	gggaagtgcc	cggtagccag	catgagccac	actaggaaag	aggaggagggt	3220
tgcagccaaa	cttaaggcac	cggcaagtgt	tgtcagcact	ggaggagacc	ccgccagtgg	3280
ggtgaggcca	gccaaagccc	tgtgttacga	atggtgggoc	aaggggctgt	ctgctaggtc	3340

187/233

cagtaggaca ggcagagctc caggctggca ccatggtagg cctccagga aagagctggg 3400
 aggcaggaat ggcacactgg gcaggcttgc ccattcctgg ccctgagaat ggagctgtag 3460
 cctcatggac aataaatgga tgtgacacc 3489

<210> 119

<211> 931

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (25)...(252)

<400> 119

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 Met Ile Gly Asp Ile Leu Leu Phe Gly

1

5

acg ttg ctg atg aat gcc ggg gcg gtg ctg aac ttt aag ctg aaa aag 99
 Thr Leu Leu Met Asn Ala Gly Ala Val Leu Asn Phe Lys Leu Lys Lys

10

15

20

25

aag gac acg cag ggc ttt ggg gag gag tcc agg gag ccc agc aca ggt 147
 Lys Asp Thr Gln Gly Phe Gly Glu Glu Ser Arg Glu Pro Ser Thr Gly

30

35

40

gac aac atc cgg gaa ttc ttg ctg agc ctc aga tac ttt cga atc ttc 195
 Asp Asn Ile Arg Glu Phe Leu Leu Ser Leu Arg Tyr Phe Arg Ile Phe

45

50

55

atc gcc ctg tgg aac atc ttc atg atg ttc tgc atg att gtg ctg ttc 243
 Ile Ala Leu Trp Asn Ile Phe Met Met Phe Cys Met Ile Val Leu Phe

60

65

70

ggc tct tgaatcccag cgatgaaacc aggaactcac tttccggga tgccgagtct c 300
 Gly Ser

75

cattcctcca ttctgatga cttcaagaat gtttttgacc agaaaacoga caaccttccc 360

agaaagtcca agctcgtggt ggggtgaaaa gtgttcgcca aggtgtgcat ggtttcccag 420

ccacgtccct gttttcaaag atagtttcac tttggtctct gaattgaaat gctgtctact 480

gaaagggttt caggagcgtt tatgtaaggg gctgtgatga aattgcattc cccatagata 540

aaagaaaaat catttctatc cagagatctg agcagaagga ttggcttgtt agtttaacac 600

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agccgtgttt ttggacattc agtggtactt gctgagtctg acagcctctg ggcccggcca 660
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 gctgcgatta accctaaagg ctttaaggaa cgggccacct gtaacagaga caccagcctt 780
 cctgtataga cactaaattg ttagcaagag tgttgagcta gttcctgggt aagtgtttcc 840
 acagaagaca tgtggagcag ttgtggggat attaaaggaa actttcctct gccttgacc 900
 ctttgttaaa taaaatgact ttgggagcca t 931

<210> 120

<211> 1123

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (68)...(547)

<400> 120

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 agtcggg atg gag ctg cct gct gtg aac ctg aag gtg att ctc cta ggt 109
 Met Glu Leu Pro Ala Val Asn Leu Lys Val Ile Leu Leu Gly
 1 5 10
 cac tgg ctg ctg aca acc tgg ggc tgc att gta ttc tca ggc tcc tat 157
 His Trp Leu Leu Thr Thr Trp Gly Cys Ile Val Phe Ser Gly Ser Tyr
 15 20 25 30
 gcc tgg gcc aac ttc acc atc ctg gcc ttg ggc gtg tgg gct gtg gct 205
 Ala Trp Ala Asn Phe Thr Ile Leu Ala Leu Gly Val Trp Ala Val Ala
 35 40 45
 cag cgg gac tcc atc gac gcc ata agc atg ttt ctg ggt ggc ttg ctg 253
 Gln Arg Asp Ser Ile Asp Ala Ile Ser Met Phe Leu Gly Gly Leu Leu
 50 55 60
 gcc acc atc ttc ctg gac atc gtg cac atc agc atc ttc tac ccg cgg 301
 Ala Thr Ile Phe Leu Asp Ile Val His Ile Ser Ile Phe Tyr Pro Arg
 65 70 75
 gtc agc ctc acg gac acg ggc cgc ttt ggc gtg ggc atg gcc atc ctc 349
 Val Ser Leu Thr Asp Thr Gly Arg Phe Gly Val Gly Met Ala Ile Leu
 80 85 90
 agc ttg ctg ctc aag ccg ctc tcc tgc tgc ttc gtc tac cac atg tac 397

189/233

Ser Leu Leu Leu Lys Pro Leu Ser Cys Cys Phe Val Tyr His Met Tyr
 95 100 105 110
 cgg gag cgc ggg ggt gag ctc ctg gtc cac act ggt ttc ctt ggg tot 445
 Arg Glu Arg Gly Gly Glu Leu Leu Val His Thr Gly Phe Leu Gly Ser
 115 120 125
 tct cag gac cgt agt gcc tac cag acg att gac tca gca gag gcg ccc 493
 Ser Gln Asp Arg Ser Ala Tyr Gln Thr Ile Asp Ser Ala Glu Ala Pro
 130 135 140
 gca gat ccc ttt gca gtc cca gag ggc agg agt caa gat gcc cga ggg 541
 Ala Asp Pro Phe Ala Val Pro Glu Gly Arg Ser Gln Asp Ala Arg Gly
 145 150 155
 tac tgaagccagc cacgctgcgc ccggccctgc cccgggcctt cctcgtgcct gggagg 600
 Tyr

tcgtttctagg gatgctcctg acctccgtct cttggacctg agatggaatg tgtccccagc 660
 tcagggattg cctgaaccaa gaggccagga gcccccatgg gccgcccagt accatgcaca 720
 ctctgtccc gaactccctg aggcctcccc tcccttcagg gcacccactg gttcccaggc 780
 tggaaccagg gtctctcttt acctcctacc ccatggtggc accacagagg ccctcagccg 840
 agtcctgcct gagtgttgca agctcaggcc tttaaggact gctgatgcc cctcaggcct 900
 cccccaagtt tgctgggctt tgggtggaagc cctgagagct tcaggctctg ctcagcccca 960
 ggagcagtct ggcatgggag tgaggccccg tccttctcac tgctgggtca catggtgcct 1020
 agggatgcag ggctggaggc cagaggtgtc agcaacactg tgaccaccca caacctccag 1080
 cctccctttt cagagcacag cattaaagtt tggggaattc tgt 1123

<210> 121

<211> 636

<212> PRT

<213> Homo sapiens

<400> 121

Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
 1 5 10 15
 Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
 20 25 30
 Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
 35 40 45

190/233

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
 50 55 60
 Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
 65 70 75 80
 Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
 85 90 95
 Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
 100 105 110
 Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
 115 120 125
 Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
 130 135 140
 Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu
 145 150 155 160
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp
 165 170 175
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro
 180 185 190
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp
 195 200 205
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile
 210 215 220
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly
 225 230 235 240
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu
 245 250 255
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro
 260 265 270
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly
 275 280 285
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala
 290 295 300
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly
 305 310 315 320
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys

191/233

325	330	335
Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly		
340	345	350
Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile		
355	360	365
Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro		
370	375	380
Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu		
385	390	395
Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu		
405	410	415
Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu		
420	425	430
Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His		
435	440	445
Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp		
450	455	460
Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val		
465	470	475
Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn		
485	490	495
Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp		
500	505	510
Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser		
515	520	525
Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Ser Ser Leu Pro Glu Thr		
530	535	540
Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr		
545	550	555
Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val		
565	570	575
Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln		
580	585	590
Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln		
595	600	605

192/233

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr
 610 615 620
 Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys
 625 630 635

<210> 122

<211> 318

<212> PRT

<213> Homo sapiens

<400> 122

Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Leu Pro Phe Leu
 1 5 10 15
 Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser Gly Val
 20 25 30
 Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg
 50 55 60
 Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly Glu Leu
 65 70 75 80
 Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val Leu Val
 85 90 95
 Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys
 100 105 110
 Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn Asn Ala
 115 120 125
 Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met
 130 135 140
 His Ile Gly Val Asn His Leu Gly His Phe Leu Leu Thr His Leu Leu
 145 150 155 160
 Leu Glu Lys Leu Lys Glu Ser Ala Pro Ser Arg Ile Val Asn Val Ser
 165 170 175
 Ser Leu Ala His His Leu Gly Arg Ile His Phe His Asn Leu Gln Gly
 180 185 190
 Glu Lys Phe Tyr Asn Ala Gly Leu Ala Tyr Cys His Ser Lys Leu Ala

193/233

195	200	205
Asn Ile Leu Phe Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly		
210	215	220
Val Thr Thr Tyr Ser Val His Pro Gly Thr Val Gln Ser Glu Leu Val		
225	230	235
Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser Phe Phe		
245	250	255
Ile Lys Thr Pro Gln Gln Gly Ala Gln Thr Ser Leu His Cys Ala Leu		
260	265	270
Thr Glu Gly Leu Glu Ile Leu Ser Gly Asn His Phe Ser Asp Cys His		
275	280	285
Val Ala Trp Val Ser Ala Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg		
290	295	300
Leu Trp Asp Val Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp		
305	310	315

<210> 123

<211> 82

<212> PRT

<213> Homo sapiens

<400> 123

Met Ala Phe Thr Leu Tyr Ser Leu Leu Gln Ala Ala Leu Leu Cys Val		
1	5	10
Asn Ala Ile Ala Val Leu His Glu Glu Arg Phe Leu Lys Asn Ile Gly		
20	25	30
Trp Gly Thr Asp Gln Gly Ile Gly Gly Phe Gly Glu Glu Pro Gly Ile		
35	40	45
Lys Ser Gln Leu Met Asn Leu Ile Arg Ser Val Arg Thr Val Met Arg		
50	55	60
Val Pro Leu Ile Ile Val Asn Ser Ile Ala Ile Val Leu Leu Leu Leu		
65	70	75
Phe Gly		80

<210> 124

194/233

<211> 247

<212> PRT

<213> Homo sapiens

<400> 124

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Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu Leu Leu
  1             5             10             15
Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu Lys Val
      20             25             30
Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg Glu Val Gly
      35             40             45
Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His Ala Gly Arg Glu
      50             55             60
Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met Gly Ser His Thr Gly
      65             70             75             80
Lys Glu Leu Asp Lys Gly Val Gln Gly Leu Asn His Gly Met Asp Lys
      85             90             95
Val Ala His Glu Ile Asn His Gly Ile Gly Gln Ala Gly Lys Glu Ala
      100            105            110
Glu Lys Leu Gly His Gly Val Asn Asn Ala Ala Gly Gln Ala Gly Lys
      115            120            125
Glu Ala Asp Lys Ala Val Gln Gly Phe His Thr Gly Val His Gln Ala
      130            135            140
Gly Lys Glu Ala Glu Lys Leu Gly Gln Gly Val Asn His Ala Ala Asp
      145            150            155            160
Gln Ala Gly Lys Glu Val Glu Lys Leu Gly Gln Gly Ala His His Ala
      165            170            175
Ala Gly Gln Ala Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn
      180            185            190
Gln Ala Ser Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser
      195            200            205
Gly Ser Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser
      210            215            220
Gly Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
      225            230            235            240
Ser Val Ala Asn Ile Met Pro

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195/233

245

<210> 125

<211> 206

<212> PRT

<213> Homo sapiens

<400> 125

Met Ala Pro Ser His Leu Ser Val Arg Glu Met Arg Glu Asp Glu Lys
 1 5 10 15
 Pro Leu Val Leu Glu Met Leu Lys Ala Gly Val Lys Asp Thr Glu Asn
 20 25 30
 Arg Val Ala Leu His Ala Leu Thr Arg Pro Pro Ala Leu Leu Leu Leu
 35 40 45
 Ala Ala Ala Ser Ser Gly Leu Arg Phe Val Leu Ala Ser Phe Ala Leu
 50 55 60
 Ala Leu Leu Leu Pro Val Phe Leu Ala Val Ala Ala Val Lys Leu Gly
 65 70 75 80
 Leu Arg Ala Arg Trp Gly Ser Leu Pro Pro Pro Gly Gly Leu Gly Gly
 85 90 95
 Pro Trp Val Ala Val Arg Gly Ser Gly Asp Val Cys Gly Val Leu Ala
 100 105 110
 Leu Ala Pro Gly Thr Asn Ala Gly Asp Gly Ala Arg Val Thr Arg Leu
 115 120 125
 Ser Val Ser Arg Trp His Arg Arg Arg Gly Val Gly Arg Arg Leu Leu
 130 135 140
 Ala Phe Ala Glu Ala Arg Ala Arg Ala Trp Ala Gly Gly Met Gly Glu
 145 150 155 160
 Pro Arg Ala Arg Leu Val Val Pro Val Ala Val Ala Ala Trp Gly Val
 165 170 175
 Gly Gly Met Leu Glu Gly Cys Gly Tyr Gln Ala Glu Gly Gly Trp Gly
 180 185 190
 Cys Leu Gly Tyr Thr Leu Val Arg Glu Phe Ser Lys Asp Leu
 195 200 205

<210> 126

196/233

<211> 432

<212> PRT

<213> Homo sapiens

<400> 126

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Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
  1              5              10              15
Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
              20              25              30
Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
              35              40              45
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
              50              55              60
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
              65              70              75              80
Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
              85              90              95
Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
              100             105             110
Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
              115             120             125
Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
              130             135             140
Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
              145             150             155             160
Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
              165             170             175
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
              180             185             190
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
              195             200             205
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
              210             215             220
Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
              225             230             235             240
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser

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197/233

	245		250		255
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu					
	260		265		270
Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp					
	275		280		285
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe					
	290		295		300
Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu					
	305		310		315
Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu					
	325		330		335
Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln					
	340		345		350
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr					
	355		360		365
Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu					
	370		375		380
Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val					
	385		390		395
Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys					
	405		410		415
Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val					
	420		425		430

<210> 127

<211> 306

<212> PRT

<213> Homo sapiens

<400> 127

Met Gly His Arg Thr Leu Val Leu Pro Trp Val Leu Leu Thr Leu Cys			
1	5	10	15
Val Thr Ala Gly Thr Pro Glu Val Trp Val Gln Val Arg Met Glu Ala			
20	25	30	
Thr Glu Leu Ser Ser Phe Thr Ile Arg Cys Gly Phe Leu Gly Ser Gly			
35	40	45	

198/233

Ser Ile Ser Leu Val Thr Val Ser Trp Gly Gly Pro Asp Gly Ala Gly
 50 55 60
 Gly Thr Thr Leu Ala Val Leu His Pro Glu Arg Gly Ile Arg Gln Trp
 65 70 75 80
 Ala Pro Ala Arg Gln Ala Arg Trp Glu Thr Gln Ser Ser Ile Ser Leu
 85 90 95
 Ile Leu Glu Gly Ser Gly Ala Ser Ser Pro Cys Ala Asn Thr Thr Phe
 100 105 110
 Cys Cys Lys Phe Ala Ser Phe Pro Glu Gly Ser Trp Glu Ala Cys Gly
 115 120 125
 Ser Leu Pro Pro Ser Ser Asp Pro Gly Leu Ser Ala Pro Pro Thr Pro
 130 135 140
 Ala Pro Ile Leu Arg Ala Asp Leu Ala Gly Ile Leu Gly Val Ser Gly
 145 150 155 160
 Val Leu Leu Phe Gly Cys Val Tyr Leu Leu His Leu Leu Arg Arg His
 165 170 175
 Lys His Arg Pro Ala Pro Arg Leu Gln Pro Ser Arg Thr Ser Pro Gln
 180 185 190
 Ala Pro Arg Ala Arg Ala Trp Ala Pro Ser Gln Ala Ser Gln Ala Ala
 195 200 205
 Leu His Val Pro Tyr Ala Thr Ile Asn Thr Ser Cys Arg Pro Ala Thr
 210 215 220
 Leu Asp Thr Ala His Pro His Gly Gly Pro Ser Trp Trp Ala Ser Leu
 225 230 235 240
 Pro Thr His Ala Ala His Arg Pro Gln Gly Pro Ala Ala Trp Ala Ser
 245 250 255
 Thr Pro Ile Pro Ala Arg Gly Ser Phe Val Ser Val Glu Asn Gly Leu
 260 265 270
 Tyr Ala Gln Ala Gly Glu Arg Pro Pro His Thr Gly Pro Gly Leu Thr
 275 280 285
 Leu Phe Pro Asp Pro Arg Gly Pro Arg Ala Met Glu Gly Pro Leu Gly
 290 295 300
 Val Arg
 305

199/233

<210> 128

<211> 555

<212> PRT

<213> Homo sapiens

<400> 128

Met Gln Ser Cys Glu Ser Ser Gly Asp Ser Ala Asp Asp Pro Leu Ser
 1 5 10 15
 Arg Gly Leu Arg Arg Arg Gly Gln Pro Arg Val Val Val Ile Gly Ala
 20 25 30
 Gly Leu Ala Gly Leu Ala Ala Ala Lys Ala Leu Leu Glu Gln Gly Phe
 35 40 45
 Thr Asp Val Thr Val Leu Glu Ala Ser Ser His Ile Gly Gly Arg Val
 50 55 60
 Gln Ser Val Lys Leu Gly His Ala Thr Phe Glu Leu Gly Ala Thr Trp
 65 70 75 80
 Ile His Gly Ser His Gly Asn Pro Ile Tyr His Leu Ala Glu Ala Asn
 85 90 95
 Gly Leu Leu Glu Glu Thr Thr Asp Gly Glu Arg Ser Val Gly Arg Ile
 100 105 110
 Ser Leu Tyr Ser Lys Asn Gly Val Ala Cys Tyr Leu Thr Asn His Gly
 115 120 125
 Arg Arg Ile Pro Lys Asp Val Val Glu Glu Phe Ser Asp Leu Tyr Asn
 130 135 140
 Glu Val Tyr Asn Leu Thr Gln Glu Phe Phe Arg His Asp Lys Pro Val
 145 150 155 160
 Asn Ala Glu Ser Gln Asn Ser Val Gly Val Phe Thr Arg Glu Glu Val
 165 170 175
 Arg Asn Arg Ile Arg Asn Asp Pro Asp Asp Pro Glu Ala Thr Lys Arg
 180 185 190
 Leu Lys Leu Ala Met Ile Gln Gln Tyr Leu Lys Val Glu Ser Cys Glu
 195 200 205
 Ser Ser Ser His Ser Met Asp Glu Val Ser Leu Ser Ala Phe Gly Glu
 210 215 220
 Trp Thr Glu Ile Pro Gly Ala His His Ile Ile Pro Ser Gly Phe Met
 225 230 235 240

200/233

Arg Val Val Glu Leu Leu Ala Glu Gly Ile Pro Ala His Val Ile Gln
 245 250 255
 Leu Gly Lys Pro Val Arg Cys Ile His Trp Asp Gln Ala Ser Ala Arg
 260 265 270
 Pro Arg Gly Pro Glu Ile Glu Pro Arg Gly Glu Gly Asp His Asn His
 275 280 285
 Asp Thr Gly Glu Gly Gly Gln Gly Gly Glu Glu Pro Arg Gly Gly Arg
 290 295 300
 Trp Asp Glu Asp Glu Gln Trp Ser Val Val Val Glu Cys Glu Asp Cys
 305 310 315 320
 Glu Leu Ile Pro Ala Asp His Val Ile Val Thr Val Ser Leu Gly Val
 325 330 335
 Leu Lys Arg Gln Tyr Thr Ser Phe Phe Arg Pro Gly Leu Pro Thr Glu
 340 345 350
 Lys Val Ala Ala Ile His Arg Leu Gly Ile Gly Thr Thr Asp Lys Ile
 355 360 365
 Phe Leu Glu Phe Glu Glu Pro Phe Trp Gly Pro Glu Cys Asn Ser Leu
 370 375 380
 Gln Phe Val Trp Glu Asp Glu Ala Glu Ser His Thr Leu Thr Tyr Pro
 385 390 395 400
 Pro Glu Leu Trp Tyr Arg Lys Ile Cys Gly Phe Asp Val Leu Tyr Pro
 405 410 415
 Pro Glu Arg Tyr Gly His Val Leu Ser Gly Trp Ile Cys Gly Glu Glu
 420 425 430
 Ala Leu Val Met Glu Lys Cys Asp Asp Glu Ala Val Ala Glu Ile Cys
 435 440 445
 Thr Glu Met Leu Arg Gln Phe Thr Gly Asn Pro Asn Ile Pro Lys Pro
 450 455 460
 Arg Arg Ile Leu Arg Ser Ala Trp Gly Ser Asn Pro Tyr Phe Arg Gly
 465 470 475 480
 Ser Tyr Ser Tyr Thr Gln Val Gly Ser Ser Gly Ala Asp Val Glu Lys
 485 490 495
 Leu Ala Lys Pro Leu Pro Tyr Thr Glu Ser Ser Lys Thr Ala Pro Met
 500 505 510
 Gln Val Leu Phe Ser Gly Glu Ala Thr His Arg Lys Tyr Tyr Ser Thr

201/233

515	520	525
Thr His Gly Ala Leu Leu Ser Gly Gln Arg Glu Ala Ala Arg Leu Ile		
530	535	540
Glu Met Tyr Arg Asp Leu Phe Gln Gln Gly Thr		
545	550	555

<210> 129

<211> 250

<212> PRT

<213> Homo sapiens

<400> 129

Met Gly Ser Gln His Ser Ala Ala Ala Arg Pro Ser Ser Cys Arg Arg			
1	5	10	15
Lys Gln Glu Asp Asp Arg Asp Gly Leu Leu Ala Glu Arg Glu Gln Glu			
20	25	30	
Glu Ala Ile Ala Gln Phe Pro Tyr Val Glu Phe Thr Gly Arg Asp Ser			
35	40	45	
Ile Thr Cys Leu Thr Cys Gln Gly Thr Gly Tyr Ile Pro Thr Glu Gln			
50	55	60	
Val Asn Glu Leu Val Ala Leu Ile Pro His Ser Asp Gln Arg Leu Arg			
65	70	75	80
Pro Gln Arg Thr Lys Gln Tyr Val Leu Leu Ser Ile Leu Leu Cys Leu			
85	90	95	
Leu Ala Ser Gly Leu Val Val Phe Phe Leu Phe Pro His Ser Val Leu			
100	105	110	
Val Asp Asp Asp Gly Ile Lys Val Val Lys Val Thr Phe Asn Lys Gln			
115	120	125	
Asp Ser Leu Val Ile Leu Thr Ile Met Ala Thr Leu Lys Ile Arg Asn			
130	135	140	
Ser Asn Phe Tyr Thr Val Ala Val Thr Ser Leu Ser Ser Gln Ile Gln			
145	150	155	160
Tyr Met Asn Thr Val Val Ser Thr Tyr Val Thr Thr Asn Val Ser Leu			
165	170	175	
Ile Pro Pro Arg Ser Glu Gln Leu Val Asn Phe Thr Gly Lys Ala Glu			
180	185	190	

202/233

Met Gly Gly Pro Phe Ser Tyr Val Tyr Phe Phe Cys Thr Val Pro Glu
 195 200 205
 Ile Leu Val His Asn Ile Val Ile Phe Met Arg Thr Ser Val Lys Ile
 210 215 220
 Ser Tyr Ile Gly Leu Met Thr Gln Ser Ser Leu Glu Thr His His Tyr
 225 230 235 240
 Val Asp Cys Gly Gly Asn Ser Thr Ala Ile
 245 250

<210> 130

<211> 174

<212> PRT

<213> Homo sapiens

<400> 130

Met Gln Ala Pro Ala Phe Arg Asp Lys Lys Gln Gly Val Ser Ala Lys
 1 5 10 15
 Asn Gln Gly Ala His Asp Pro Asp Tyr Glu Asn Ile Thr Leu Ala Phe
 20 25 30
 Lys Asn Gln Asp His Ala Lys Gly Gly His Ser Arg Pro Thr Ser Gln
 35 40 45
 Val Pro Ala Gln Cys Arg Pro Pro Ser Asp Ser Thr Gln Val Pro Cys
 50 55 60
 Trp Leu Tyr Arg Ala Ile Leu Ser Leu Tyr Ile Leu Leu Ala Leu Ala
 65 70 75 80
 Phe Val Leu Cys Ile Ile Leu Ser Ala Phe Ile Met Val Lys Asn Ala
 85 90 95
 Glu Met Ser Lys Glu Leu Leu Gly Phe Lys Arg Glu Leu Trp Asn Val
 100 105 110
 Ser Asn Ser Val Gln Ala Cys Glu Glu Arg Gln Lys Arg Gly Trp Asp
 115 120 125
 Ser Val Gln Gln Ser Ile Thr Met Val Arg Ser Lys Ile Asp Arg Leu
 130 135 140
 Glu Thr Thr Leu Ala Gly Ile Lys Asn Ile Asp Thr Lys Val Gln Lys
 145 150 155 160
 Ile Leu Glu Val Leu Gln Lys Met Pro Gln Ser Ser Pro Gln

203/233

165

170

<210> 131

<211> 1908

<212> DNA

<213> Homo sapiens

<400> 131

atgaccacgt ggagcctccg gcggaggccg gcccgcacgc tgggactcct gctgctggtc	60
gtcttgggct tcttgggtct tcgcaggctg gactggagca ccttgggtccc tctgcggctc	120
cgccatcgac agctggggct gcaggccag ggctggaaact tcatgctgga ggattccacc	180
ttctggatct tcgggggctc catccactat ttccgtgtgc ccaggagta ctggaggagc	240
cgcctgctga agatgaagga ctgtggcttg aacacootca ccacctatgt tccgtggaac	300
ctgcatgagc cagaaagagg caaatttgac ttctctggga acctggacct ggaggccttc	360
gtcctgatgg ccgcagagat cgggctgtgg gtgattctgc gtccaggccc ctacatctgc	420
agtgagatgg acctcggggg cttgccacgc tggctactcc aagaccttg catgaggctg	480
aggacaactt acaagggett caccgaagca gtggaccttt attttgacca cctgatgtcc	540
agggtggtgc cactccagta caagcgtggg ggacctatca ttgacctgca ggtggagaat	600
gaatatggtt cctataataa agaccccgca tacatgccct acgtcaagaa ggcactggag	660
gacctgtgca ttgtggaact gctcctgact tcagacaaca aggatgggct gagcaagggg	720
attgtccagg gagtcttggc caccatcaac ttgcagtcaa cacacgagct gcagctactg	780
accaccttcc tcttcaacgt ccaggggact cagcccaaga tggatgatga gtactggagc	840
gggttggttg actcgtgggg aggccctcac aatatcttgg attcttctga ggttttgaaa	900
acogtgtctg ccattgtgga cgccggctcc tccatcaacc totacatgtt ccacggaggc	960
accaactttg gcttcatgaa tggagccatg cacttccatg actacaagtc agatgtcacc	1020
agctatgact atgatgctgt gctgacagaa gccggcgatt acacggccaa gtacatgaag	1080
cttcgagact tcttcggctc catctcaggc atccctctcc ctccccacc tgaccttctt	1140
cccaagatgc cgtatgagcc cttaacgcca gtcttgtaac tgtctctgtg ggacgccctc	1200
aagtacctgg gggagccaat caagtctgaa aagcccatca acatggagaa cctgccagtc	1260
aatgggggaa atggacagtc cttcgggtac attctctatg agaccagcat cacctcgtct	1320
ggcatcctca gtggccacgt gcatgatcgg gggcagggtg ttgtgaacac agtatccata	1380
ggattcttgg actacaagac aacgaagatt gctgtccccc tgatccaggg ttacaccgtg	1440
ctgaggatct tgggtggagaa tcgtgggcga gtcaactatg gggagaatat tgatgaccag	1500
cgcaaaggct taattggaaa tctctatctg aatgattcac cctgaaaaa cttcagaatc	1560
tatagcctgg atatgaagaa gagcttcttt cagaggttcg gcctggacaa atggagttcc	1620
ctcccagaaa caccacatt acctgcttcc ttcttgggta gcttgtccat cagctccacc	1680

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ccttgtgaca cctttctgaa gctggagggc tgggagaagg gggttgtatt catcaatggc 1740
 cagaaccttg gacgttactg gaacattgga ccccaagaaga cgctttacct ccaggtccc 1800
 tgggttgagca gcggaatcaa ccaggtcacc gtttttgagg agacgatggc gggccctgca 1860
 ttacagttca cggaaacccc ccacctgggc aggaaccagt acattaag 1908

<210> 132

<211> 954

<212> DNA

<213> Homo sapiens

<400> 132

atggttgagc toatgttccc gctgttgctc ctccctctgc ccttccttct gtatatggct 60
 gcgccccaaa tcaggaaaat gctgtccagt ggggtgtgta catcaactgt tcagcttcct 120
 gggaaagtag ttgtggtcac aggagctaat acaggtatcg ggaaggagac agccaaagag 180
 ctggttcaga gaggagctcg agtatattta gcttgccggg atgtggaaaa gggggaattg 240
 gtggccaaag agatccagac caccgacaggg aaccagcagg tgttggtgcg gaaactggac 300
 ctgtctgata ctaagtctat tcgagctttt gctaagggtc tcttagctga ggaaaagcac 360
 ctccacgttt tgatcaacaa tgcaggagtg atgatgtgct cgtactcgaa gacagcagat 420
 ggctttgaga tgcacatagg agtcaaccac ttgggtcact tcctcctaac ccatctgctg 480
 ctagagaaac taaaggaatc agccccatca aggatagtaa atgtgtcttc cctcgcacat 540
 cacctgggaa ggatccactt ccataacctg cagggcgaga aattctacaa tgcaggcctg 600
 gcctactgtc acagcaagct agccaacatc ctcttcaccc aggaactggc ccggagacta 660
 aaaggctctg gcgttacgac gtattotgta caccctggca cagtccaatc tgaactggtt 720
 cggcactcat ctttcatgag atggatgtgg tggcttttct cctttttcat caagactcct 780
 cagcagggag cccagaccag cctgcactgt gcottaacag aaggctctga gattctaagt 840
 gggaaatcatt tcagtgactg tcatgtggca tgggtctctg cccaagctcg taatgagact 900
 atagcaaggc ggctgtggga cgtcagttgt gacctgctgg gcctcccaat agac 954

<210> 133

<211> 246

<212> DNA

<213> Homo sapiens

<400> 133

atggccttta cctgttactc actgctgcag gcagccctgc totgcgtcaa cgccatcgca 60
 gtgtgtcacg aggagcgatt cctcaagaac attggctggg gaacagacca ggggaattggt 120
 ggatttgag aagagccggg aattaaatca cagctaataa accttattcg atctgtaaga 180

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accgtgatga gagtgccatt gataatagta aactcaattg caattgtgtt acttttatta 240
 tttgga 246

<210> 134

<211> 741

<212> DNA

<213> Homo sapiens

<400> 134

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 ggatggggcg ccagcgatga cccattgag aaggtcattg aagggatcaa ccgagggctg 120
 agcaatgcag agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcac 180
 gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag ccacaccggc 240
 aaggagttag acaaaggcgt ccaggggctc aaccacggca tggacaaggt tgcccatgag 300
 atcaaccatg gtattggaca agcaggaaa gaaagcagaga agcttggcca tgggggtcaac 360
 aacgctgctg gacaggccgg gaaggaagca gacaaagcgg tccaagggtt ccacactggg 420
 gtccaccagg ctgggaagga agcagagaaa cttggccaag gggtaacca tgctgctgac 480
 caggctggaa aggaagtgga gaagcttggc caaggtgccc accatgctgc tggccaggcc 540
 gggaaggagc tgcaaatgc tcataatggg gtcaaccaag ccagcaagga ggccaaccag 600
 ctgctgaatg gcaaccatca aagcggatct tccagccatc aaggaggggc cacaaccacg 660
 ccgttagcct ctggggcctc ggtcaacacg cctttcatca accctccgcg cctgtggagg 720
 agcgtcgcca acatcatgcc c 741

<210> 135

<211> 618

<212> DNA

<213> Homo sapiens

<400> 135

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 gagatgctga aggcggcgt gaaggacacg gaaaaccgcg tggccctcca tgccttgaca 120
 cggccgcgg ccctgctcct cctggcggcg gccagcagcg gcctgcgctt tgcctggct 180
 tccttcgccc tggccctcct cctgcgggtg ttcctggctg tggccgccgt gaagctgggc 240
 ctgcggggcc gatggggctc gctgcctccg ccgggtggcc tggggggccc ctgggtggcc 300
 gtgcggggct ccgggtgacg gtgtggggct ctggctctgg ccctggcac aaatgcaggg 360
 gacggggccc gggtaaccgg cctgtctgtc tctcgtggc accgcgcgcg gggcgtgggc 420
 aggaggtgc tggccttcgc ggagggcccg gctcgggcct gggctgggg catgggggag 480

206/233

ccccggggccc ggctcgtggt ccccggtggt gtggccgcct ggggggtggg agggatgctg 540
 gagggctgtg gctaccagge cgaggggggc tggggctgcc tgggctacac gctggtgagg 600
 gaattcagca aagacctg 618

<210> 136

<211> 1296

<212> DNA

<213> Homo sapiens

<400> 136

atggacgcca gatggtgggc agtgggtggt ctggtgcgt tccccccct aggggcaggt 60
 ggggagactc ccgaagcccc tccggagtca tggaccagc tatggttctt ccgatttgtg 120
 gtgaatgctg ctggctatgc cagctttatg gtacctggt acctcctggt gcagtacttc 180
 aggcggaaga actacctgga gaccggtagg ggccctctgt tccccctggt gaaagcttgt 240
 gtgtttggca atgagcccaa ggcctctgat gaggttcccc tggcgccccg aacagaggcg 300
 gcagagacca ccccgatgtg gcaggccctg aagctgctct tctgtgccac agggctccag 360
 gtgtcttctc tgacttgggg tgtgctgcag gaaagagtga tgaccgcag ctatggggcc 420
 acagccacat caccgggtga gcctttacg gactcgaggt tccctggtgt aatgaaccga 480
 gtgctggcac tgattgtggc tggcctctcc tgtgttctct gcaagcagcc ccggcatggg 540
 gcacccatgt accggctact ctttgcagc ctgtccaatg tgcttagcag ctggtgcca 600
 tacgaagctc ttaagttcgt cagcttcccc acccaggtgc tggccaaggc ctotaagggtg 660
 atccctgtca tgctgatggg aaagcttgtg tctcggcgca gctacgaaca ctgggagtac 720
 ctgacagcca cactcatctc cattggggtc agcatgttct tgctatccag cggaccagag 780
 ccccgagct cccagccac cacactctca ggcctcatct tactggcagg ttatattgct 840
 tttgacagct tcacctcaaa ctggcaggat gccctgtttg cctataagat gtcacoggtg 900
 cagatgatgt ttgggggtcaa tttctctcc tgcctcttca cagtgggtc actgctagaa 960
 cagggggccc tactggaggg aaccgccttc atggggcgac acagtgagtt tgctgcccac 1020
 gccctgctac tctccatctg ctccgcatgt ggccagctct tcatctttta caccattggg 1080
 cagtttgggg ctgccgtctt caccatctc atgacctcc gccaggcctt tgccatcctt 1140
 ctttctgccc ttctctatgg ccacactgtc actgtggtgg gagggctggg ggtggtgtg 1200
 gtctttgtg cctcctgct cagagctctac gcgcggggcc gtctaaagca acggggaaag 1260
 aaggtgtgc ctgttgagtc tctgtgcag aaggtt 1296

<210> 137

<211> 918

<212> DNA

207/233

<213> Homo sapiens

<400> 137

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accccgaggg tgtgggttca agttcgatg gaggccaccg agctctcgtc cttoaccatc     120
cgttgtgggt tcctggggtc tggctccatc tccctggtga ctgtgagctg ggggggcccc     180
gacggtgctg gggggaccac gctggctgtg ttgcaccag aacgtggcat ccggcaatgg     240
gccctgctc gccaggcccg ctgggaaacc cagagcagca totctctcat cctggaaggc     300
tctggggcca gcagccctg cgccaacacc accttctgct gcaagtttgc gtccttcctt     360
gagggtcctt gggaggcctg tgggagcctc ccgcccagct cagaccaggg gctctctgcc     420
ccgcccactc ctgcccocat tctgcgggca gacctggccg ggatcttggg ggtctcagga     480
gtcctcctct ttggtgtgt ctacctcctt catctgctgc gccacataa gcaccgccct     540
gcccttaggc tccagccgtc ccgcaccagc cccagggcac cgagagcacg agcatgggca     600
ccaagccagg cctcccaggc tgctcttcac gtcccttatg ccactatcaa caccagctgc     660
cgcccagcta ctttggaacac agtcacccc catggggggc cgtcctggtg ggcgtcactc     720
ccccccacg ctgcacaccg gcccagggc cctgcgcctt gggcctccac acctatccct     780
gcacgtggca gctttgtctc tgttgagaat ggactctacg ctcaggcagg ggagaggcct     840
ctcacactg gtcccggcct cactcttttc cctgaccctc gggggcccag ggccatggaa     900
ggacccttag gagttcga                                     918

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<210> 138

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 138

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atgcaaagtt gtgaatccag tggtgacagt ggggatgacc ctctcagtcg cggcctacgg      60
agaagggggac agcctcgtgt ggtggtgatc ggcgcgggct tggctggcct ggctgcagcc     120
aaagcacttc ttgagcaggg ttacacggat gtcactgtgc ttgaggcttc cagccacatc     180
ggaggccgtg tgcagagtgt gaaacttgga cagccacact ttgagctggg agccacctgg     240
atccatggct cccatgggaa ccctatctat catctagcag aagccaacgg cctcctggaa     300
gagacaaccg atggggaacg cagcgtgggc cgcacagcc tctattccaa gaatggcgtg     360
gcctgtacc ttaccaacca cggccgcagg atccccaagg acgtggttga ggaattcagc     420
gatttataca acgaggtcta taacttgacc caggagttct tccggcacga taaaccagtc     480
aatgtgaaa gtcaaatag cgtgggggtg ttcacccgag aggaggtgcg taaccgcac     540
aggaatgacc ctgacgaccc agaggctacc aagcgcctga agctcgccat gatccagcag     600
tacctgaagg tggagagctg tgagagcagc tcacacagca tggacgaggt gtccttgagc     660

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gccttcgggg agtggaccga gatccccggc gctcaccaca tcatcccctc gggcttcatg 720
 cgggttgtgg agctgctggc ggagggcatc cctgcccacg tcatccagct agggaaacct 780
 gtccgctgca ttcactggga ccaggcctca gcccgcacca gaggccctga gattgagccc 840
 cggggtgagg gcgaccacaa tcacgacaact ggggaggggtg gccaggggtg agaggagccc 900
 cgggggggca ggtgggatga ggatgagcag tggtcgggtg tggaggagtg cgaggactgt 960
 gagctgatcc cggcggacca tgtgattgtg accgtgtcgc taggtgtgct aaagaggcag 1020
 tacaccagtt tcttcgggcc aggcctgccc acagagaagg tggctgccat ccaccgcctg 1080
 ggcattggca ccaccgacaa gatctttctg gaattcgagg agcccttctg gggccctgag 1140
 tgcaacagcc tacagtttgt gtgggaggac gaagcggaga gccacaccct cacctaccca 1200
 cctgagctct ggtaccgcaa gatctgcggc tttgatgtcc totaccgcc tgagcgtac 1260
 ggccatgtgc tgagcggctg gatctgcggg gaggaggccc tcgtcatgga gaagtgtgat 1320
 gacgaggcag tggccgagat ctgcacggag atgtgcgtc agttcacagg gaacccaac 1380
 attccaaac ctccggcaat cttgcgtcgc gcctggggca gcaaccotta cttccggggc 1440
 tcctattcat acacgcaggt gggctccagc gggcgggatg tggagaagct ggccaagccc 1500
 ctgccgtaca cggagagctc aaagacagcg cccatgcagg tgcgttttcc cggtagggcc 1560
 acccaccgca agtactatcc caccaccac ggtgctctgc tgtccggcca gcgtgaggct 1620
 gcccgctca ttgagatgta ccgagacctc ttccagcagg ggacc 1665

<210> 139

<211> 750

<212> DNA

<213> Homo sapiens

<400> 139

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 gacaggggacg gtttgctggc tgaacgagag caggaagaag ccattgctca gttcccatat 120
 gtggaattca ccgggagaga tagcatcacc tgtctcacgt gccaggggac aggtacatt 180
 ccaacagagc aagtaaatga gttggtggct ttgatccac acagtgatca gagattgcgc 240
 cctcagcgaa ctaagcaata tgtcctcctg tccatcctgc tttgtctcct ggcattctgt 300
 ttggtggttt tcttcctggt tccgcattca gtcottgtgg atgatgacgg catcaaagt 360
 gtgaaagtca catttaataa gcaagactcc cttgtaattc tcaccatcat ggccaccctg 420
 aaaatcagga actccaactt ctacacgggtg gcagtgacca gcctgtccag ccagattcag 480
 tacatgaaca cagtggtcag tacatatgtg actactaacg tctcccttat tccacctcgg 540
 agtgagcaac tggatgaattt taccgggaag gccgagatgg gaggaccgtt ttccatgtg 600
 tacttctctc gcacgggtacc tgagatcctg gtgcacaaca tagtgatctt catgogaact 660
 tcagtgaaga ttcatatcat tggcctcatg acccagagct ccttggagac acatcactat 720

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gtggattgtg gaggaaattc cacagctatt

750

<210> 140

<211> 522

<212> DNA

<213> Homo sapiens

<400> 140

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atgcaagcac cagccttcag ggacaagaaa caggggggtct cagccaagaa tcaagggtgcc      60
catgacccag actatgagaa tatcaccttg gccttcaaaa atcaggacca tgcaaaggggt      120
ggtcattcac gaccacagag ccaagtccca gccagtgca ggccgcctc agactccacc      180
caggccccct gctggttgta cagagccatc ctgagcctgt acatcctcct ggccctggcc      240
tttgtcctct gcatcatcct gtcagccttc atcatggtga agaattgctga gatgtccaag      300
gagctgctgg gctttaaaag ggagctttgg aatgtctcaa actccgtaca agcatgcgaa      360
gagagacaga agagaggctg ggattccgtt cagcagagca tcaccatggc caggagcaag      420
attgatagat tagagacgac attagcaggc ataaaaaaca ttgacacaaa ggtacagaaa      480
atcttgaggg tgctgcagaa aatgccacag tcttcacctc aa                          522

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<210> 141

<211> 3234

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (129)...(2039)

<400> 141

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aatgagcgcc ggcgggccgg ttgccaggc gaccagcgcg cggctccgcc cccgcggcg      60
aggctccgc gcgcggctga gtgcggactg gagtgggaac cgggtcccc gcgcttagag      120
aacacgcg atg acc acg tgg agc ctc cgg cgg agg ccg gcc cgc acg ctg      170
      Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu
            1             5             10
gga ctc ctg ctg ctg gtc gtc ttg ggc ttc ctg gtg ctt cgc agg ctg      218
Gly Leu Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu
      15             20             25             30
gac tgg agc acc ctg gtc cct ctg cgg ctc cgc cat cga cag ctg ggg      266
Asp Trp Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly

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35	40	45	
ctg cag gcc aag ggc tgg aac ttc atg ctg gag gat tcc acc ttc tgg			314
Leu Gln Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp			
50	55	60	
atc ttc ggg ggc tcc atc cac tat ttc cgt gtg ccc agg gag tac tgg			362
Ile Phe Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp			
65	70	75	
agg gac cgc ctg ctg aag atg aag gcc tgt ggc ttg aac acc ctc acc			410
Arg Asp Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr			
80	85	90	
acc tat gtt ccg tgg aac ctg cat gag cca gaa aga ggc aaa ttt gac			458
Thr Tyr Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp			
95	100	105	110
ttc tct ggg aac ctg gac ctg gag gcc ttc gtc ctg atg gcc gca gag			506
Phe Ser Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu			
115	120	125	
atc ggg ctg tgg gtg att ctg cgt cca ggc ccc tac atc tgc agt gag			554
Ile Gly Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu			
130	135	140	
atg gac ctc ggg ggc ttg ccc agc tgg cta ctc caa gac cct ggc atg			602
Met Asp Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met			
145	150	155	
agg ctg agg aca act tac aag ggc ttc acc gaa gca gtg gac ctt tat			650
Arg Leu Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr			
160	165	170	
ttt gac cac ctg atg tcc agg gtg gtg cca ctc cag tac aag cgt ggg			698
Phe Asp His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly			
175	180	185	190
gga cct atc att gcc gtg cag gtg gag aat gaa tat ggt tcc tat aat			746
Gly Pro Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn			
195	200	205	
aaa gac ccc gca tac atg ccc tac gtc aag aag gca ctg gag gac cgt			794
Lys Asp Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg			
210	215	220	
ggc att gtg gaa ctg ctc ctg act tca gac aac aag gat ggg ctg agc			842

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Gly Ile Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser	
225 230 235	
aag ggg att gtc cag gga gtc ttg gcc acc atc aac ttg cag tca aca	890
Lys Gly Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr	
240 245 250	
cac gag ctg cag cta ctg acc acc ttt ctc ttc aac gtc cag ggg act	938
His Glu Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr	
255 260 265 270	
cag ccc aag atg gtg atg gag tac tgg acg ggg tgg ttt gac tcg tgg	986
Gln Pro Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp	
275 280 285	
gga ggc cct cac aat atc ttg gat tct tct gag gtt ttg aaa acc gtg	1034
Gly Gly Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val	
290 295 300	
tct gcc att gtg gac gcc ggc tcc tcc atc aac ctc tac atg ttc cac	1082
Ser Ala Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His	
305 310 315	
gga ggc acc aac ttt ggc ttc atg aat gga gcc atg cac ttc cat gac	1130
Gly Gly Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp	
320 325 330	
tac aag tca gat gtc acc agc tat gac tat gat gct gtg ctg aca gaa	1178
Tyr Lys Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu	
335 340 345 350	
gcc ggc gat tac acg gcc aag tac atg aag ctt cga gac ttc ttc ggc	1226
Ala Gly Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly	
355 360 365	
tcc atc tca ggc atc cct ctc cct ccc cca cct gac ctt ctt ccc aag	1274
Ser Ile Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys	
370 375 380	
atg ccg tat gag ccc tta acg cca gtc ttg tac ctg tct ctg tgg gac	1322
Met Pro Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp	
385 390 395	
gcc ctc aag tac ctg ggg gag cca atc aag tct gaa aag ccc atc aac	1370
Ala Leu Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn	
400 405 410	

atg gag aac ctg cca gtc aat ggg gga aat gga cag tcc ttc ggg tac		1418	
Met Glu Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr			
415	420	425	430
att ctc tat gag acc agc atc acc tcg tct ggc atc ctc agt ggc cac		1466	
Ile Leu Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His			
	435	440	445
gtg cat gat cgg ggg cag gtg ttt gtg aac aca gta tcc ata gga ttc		1514	
Val His Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe			
	450	455	460
ttg gac tac aag aca acg aag att gct gtc ccc ctg atc cag ggt tac		1562	
Leu Asp Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr			
	465	470	475
acc gtg ctg agg atc ttg gtg gag aat cgt ggg cga gtc aac tat ggg		1610	
Thr Val Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly			
	480	485	490
gag aat att gat gac cag cgc aaa ggc tta att gga aat ctc tat ctg		1658	
Glu Asn Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu			
495	500	505	510
aat gat tca ccc ctg aaa aac ttc aga atc tat agc ctg gat atg aag		1706	
Asn Asp Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys			
	515	520	525
aag agc ttc ttt cag agg ttc ggc ctg gac aaa tgg agt tcc ctc cca		1754	
Lys Ser Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Ser Ser Leu Pro			
	530	535	540
gaa aca ccc aca tta cct gct ttc ttc ttg ggt agc ttg tcc atc agc		1802	
Glu Thr Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser			
	545	550	555
tcc acc cct tgt gac acc ttt ctg aag ctg gag ggc tgg gag aag ggg		1850	
Ser Thr Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly			
	560	565	570
gtt gta ttc atc aat ggc cag aac ctt gga cgt tac tgg aac att gga		1898	
Val Val Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly			
575	580	585	590
ccc cag aag acg ctt tac ctc cca ggt ccc tgg ttg agc agc gga atc		1946	
Pro Gln Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile			

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595	600	605	
aac cag gtc atc gtt ttt gag gag acg atg gcg ggc cct gca tta cag			1994
Asn Gln Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln			
610	615	620	
ttc acg gaa acc ccc cac ctg ggc agg aac cag tac att aag tgag			2040
Phe Thr Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys			
625	630	635	
cggtggcacc ccctcctgct ggtgccagtg ggagactgcc gcctcctctt gacctgaagc			2100
ctggtggctg ctgccccacc cctcactgca aaagcatctc cttaagtagc aacctcaggg			2160
actgggggct acagtctgcc cctgtctcag ctcaaaaccc taagcctgca gggaaaggtg			2220
ggatggctct gggcctggct ttgttgatga tggttttctt acagccctgc tcttgtgccg			2280
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gactcaggcg tgccttttgc tggttcctgg gaggttggc cacatccctc atggcccat			2460
tttatccccg aaatcctggg tgtgtcacca gtgtagaggg tggggaaggg gtgtctcacc			2520
tgagctgact ttgttcttcc ttcacaacct tctgagcctt ctttgggatt ctggaaggaa			2580
ctcgcggtga gaaacatgtg acttccccct tcccttccca ctgctgctt cccacagggg			2640
gacaggctgg gctggagaaa cagaaatcct caccctgcgt cttcccaagt tagcagggtg			2700
ctctggtgtt cagtggaggag gacatgtgag tcctggcaga agccatggcc catgtctgca			2760
catccaggga ggaggacaga aggccagct cacatgtgag tcctggcaga agccatggcc			2820
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agccatggcc catgtctgca catccaggga ggaggacaga aggccagct cacatgtgag			2940
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cacatgtgag tcctggcaga agccatggcc catgtctgca catccaggga ggaggacaga			3060
agggccagct cagtggcccc cgcctccac ccccccacgc cgaacagcag gggcagagca			3120
gccctccttc gaagtgtgtc caagtccgca tttgagcctt gttctggggc ccagcccaac			3180
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<210> 142

<211> 2490

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)...(1026)

214/233

<400> 142

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ccggcagag atg gtt gag ctg atg ttc ccg ctg ttg ctg ctg ctt ctg ccc      111
      Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Leu Pro
              1              5              10
ttc ctt ctg tat atg gct gcg ccc caa atc agg aaa atg ctg tcc agt      159
Phe Leu Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser
      15              20              25              30
ggg gtg tgt aca tca act gtt cag ctt cct ggg aaa gta gtt gtg gtc      207
Gly Val Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val
              35              40              45
aca gga gct aat aca ggt atc ggg aag gag aca gcc aaa gag ctg gct      255
Thr Gly Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala
              50              55              60
cag aga gga gct cga gta tat tta gct tgc cgg gat gtg gaa aag ggg      303
Gln Arg Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly
              65              70              75
gaa ttg gtg gcc aaa gag atc cag acc acg aca ggg aac cag cag gtg      351
Glu Leu Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val
              80              85              90
ttg gtg cgg aaa ctg gac ctg tot gat act aag tot att cga gct ttt      399
Leu Val Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe
      95              100              105              110
gct aag ggc ttc tta gct gag gaa aag cac ctg cac gtt ttg atc aac      447
Ala Lys Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn
              115              120              125
aat gca gga gtg atg atg tgt ccg tac tog aag aca gca gat ggc ttt      495
Asn Ala Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe
              130              135              140
gag atg cac ata gga gtc aac cac ttg ggt cac ttc ctg cta acc cat      543
Glu Met His Ile Gly Val Asn His Leu Gly His Phe Leu Leu Thr His
              145              150              155
ctg ctg cta gag aaa cta aag gaa tca gcc cca tca agg ata gta aat      591
Leu Leu Leu Glu Lys Leu Lys Glu Ser Ala Pro Ser Arg Ile Val Asn
              160              165              170

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[illegible]

216/233

atcaccggag gtcagtagtt caagaccagc ctggccaaca tggtgaaacc ccacctctac 1560
 taaaaattgt gtatatcttt gtgtgtcttc ctgtttatgt gtgccaaggg agtattttca 1620
 caaagttcaa aacagccaca ataatcagag atggagcaaa ccagtgccat ccagtcttta 1680
 tgcaaatgaa atgctgcaaa ggggaagcaga ttctgtatat gttggtaact acccaccaag 1740
 agcacatggg tagcagggaa gaagtaaaaa aagagaagga gaatactgga agataatgca 1800
 caaaatgaag ggactagtta aggattaact agccctttaa ggattaacta gttaaggatt 1860
 aatagcaaaa gatattaaat atgctaacat agctatggag gaattgaggg caagcaccca 1920
 ggactgatga ggtcttaaca aaaaccagtg tggcaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
 aaaaaaatcc taaaaacaaa caaacaaaaa aaacaattct tcattcagaa aaattatctt 2040
 agggactgat attggttaatt atgggtcaatt taataatatt ttggggcatt tccttacatt 2100
 gtcttgacaa gattaaaatg tctgtgcaa aattttgtat tttatttgga gacttcttat 2160
 caaaagtaat gctgccaaag gaagtctaag gaattagtag tgttcccatc acttgtttg 2220
 agtgtgctat tctaaaagat tttgatttcc tggaatgaca attatatttt aactttggtg 2280
 ggggaaagag ttataggacc acagtcttca cttotgatac ttgtaaatta atcttttatt 2340
 gcacttgttt tgaccattaa gctatatgtt tagaaatggt cattttacgg aaaaattaga 2400
 aaaattctga taatagtgca gaataaatga attaatgttt tacttaattt atattgaact 2460
 gtcaatgaca aataaaaatt ctttttgatt 2490

<210> 143

<211> 1465

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (84)...(332)

<400> 143

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 ctteggggcg gctcgggacg gcc atg gcc ttt acc ctg tac tca ctg ctg 110
 Met Ala Phe Thr Leu Tyr Ser Leu Leu
 1 5
 cag gca gcc ctg ctc tgc gtc aac gcc atc gca gtg ctg cac gag gag 158
 Gln Ala Ala Leu Leu Cys Val Asn Ala Ile Ala Val Leu His Glu Glu
 10 15 20 25
 cga ttc ctc aag aac att ggc tgg gga aca gac cag gga att ggt gga 206
 Arg Phe Leu Lys Asn Ile Gly Trp Gly Thr Asp Gln Gly Ile Gly Gly

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30	35	40	
ttt gga gaa gag ccg gga att aaa tca cag cta atg aac ctt att cga			254
Phe Gly Glu Glu Pro Gly Ile Lys Ser Gln Leu Met Asn Leu Ile Arg			
45	50	55	
tct gta aga acc gtg atg aga gtg cca ttg ata ata gta aac tca att			302
Ser Val Arg Thr Val Met Arg Val Pro Leu Ile Ile Val Asn Ser Ile			
60	65	70	
gca att gtg tta ctt tta tta ttt gga tgaatatcag tggagaaaat g			350
Ala Ile Val Leu Leu Leu Leu Phe Gly			
75	80		
gagactcaga agaggacatg ccagtagaag ttattacttt ggtcattatt ggaatattta			410
tatcttagct ggctgacott gcacttgtaaaaatgtaaa gctgaaaata aaaccaggggt			470
ttctatttat ctgttttttt ttttaattgtt gcacttgtag ttctattaca aaagatcaga			530
tcatgaaagg cagtaactct ccaggactgg aatatctgat tgctcagtgt taatagtagt			590
tcagtctgtg gtgagattgt taaaagggtg caagactgtt gcttctcttt ttttagatat			650
ttttctatct ctcaactctc agggatgaaa ttctttttca aagttttgaa gttccttgca			710
acttagccat gatgtgagtg gttatcccta gataaaatta aaaggatttt taaaaagtaa			770
ttactgcaca taaaatgata aataggtaat ttgaataatt ttattttaag ctccctgggt			830
aattatttttg tctattgtct cagctataaa ttcaaattta tacatactat tgagtattaa			890
tattctctga ttccaggag aattctgtca gtcacatgat gattatgttt ttgtttaaca			950
ttctttccat gcacttgta ttttattaat ttgcctgaat gatgagacca gaccagtgtc			1010
tacagatttt cattgtcaga aaaatctata agtctgcct ttttacaatg atgatttaaa			1070
aaaaacaaca gcgtaaatat tagcccacaa ggcagtcct aaacaatcac aattacactg			1130
tactacccaa gaagactgtt tattgtgaag catttacott tcaaaaaatc attacatttc			1190
tattttcttg tggagcagca cattgtggag tgtgattctt aattcttcat tgagtttgtc			1250
aataggacat tgatgtgga taggttgtct tttgttttta tgtctcagac catcttgta			1310
gattgtttgc ctatctcata atacagtttt atgcagaaag gttgaaacta tgtaaatggt			1370
ttttatggaa attatcagtt acaatatttt aaaggtgtag aatggcatct ttgtttatag			1430
gagaacattt gtaaataaag ttaaatttct aagtc			1465

<210> 144

<211> 917

<212> DNA

<213> Homo sapiens

<220>

218/233

<221> CDS

<222> (32)...(775)

<400> 144

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tctctgcatac ctcccgacc ttccagcaa t atg cat ctt gca cgt ctg gtc      52
                               Met His Leu Ala Arg Leu Val
                               1           5

ggc tcc tgc tcc ctc ctt ctg cta ctg ggg gcc ctg tct gga tgg gcg      100
Gly Ser Cys Ser Leu Leu Leu Leu Leu Gly Ala Leu Ser Gly Trp Ala
          10           15           20

gcc agc gat gac ccc att gag aag gtc att gaa ggg atc aac cga ggg      148
Ala Ser Asp Asp Pro Ile Glu Lys Val Ile Glu Gly Ile Asn Arg Gly
          25           30           35

ctg agc aat gca gag aga gag gtg ggc aag gcc ctg gat ggc atc aac      196
Leu Ser Asn Ala Glu Arg Glu Val Gly Lys Ala Leu Asp Gly Ile Asn
          40           45           50           55

agt gga atc acg cat gcc gga agg gaa gtg gag aag gtt ttc aac gga      244
Ser Gly Ile Thr His Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly
          60           65           70

ctt agc aac atg ggg agc cac acc ggc aag gag ttg gac aaa ggc gtc      292
Leu Ser Asn Met Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val
          75           80           85

cag ggg ctc aac cac ggc atg gac aag gtt gcc cat gag atc aac cat      340
Gln Gly Leu Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His
          90           95           100

ggt att gga caa gca gga aag gaa gca gag aag ctt ggc cat ggg gtc      388
Gly Ile Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val
          105           110           115

aac aac gct gct gga cag gcc ggg aag gaa gca gac aaa gcg gtc caa      436
Asn Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln
          120           125           130           135

ggg ttc cac act ggg gtc cac cag gct ggg aag gaa gca gag aaa ctt      484
Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys Leu
          140           145           150

ggc caa ggg gtc aac cat gct gct gac cag gct gga aag gaa gtg gag      532
Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu Val Glu

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219/233

155	160	165	
aag ctt ggc caa ggt gcc cac cat gct gct ggc cag gcc ggg aag gag			580
Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala Gly Lys Glu			
170	175	180	
ctg cag aat gct cat aat ggg gtc aac caa gcc agc aag gag gcc aac			628
Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser Lys Glu Ala Asn			
185	190	195	
cag ctg ctg aat ggc aac cat caa agc gga tct tcc agc cat caa gga			676
Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser Ser Ser His Gln Gly			
200	205	210	215
ggg gcc aca acc acg ccg tta gcc tct ggg gcc tcg gtc aac acg cct			724
Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly Ala Ser Val Asn Thr Pro			
220	225	230	
ttc atc aac ctt ccc gcc ctg tgg agg agc gtc gcc aac atc atg ccc			772
Phe Ile Asn Leu Pro Ala Leu Trp Arg Ser Val Ala Asn Ile Met Pro			
235	240	245	
taaactgg catccggcct tgctgggaga ataatgtcgc cgttgtcaca tcagctgaca			830
tgacctggag ggggtggggg tgggggacag gtttctgaaa tccctgaagg gggttgtact			890
gggatttgtg aataaaacttg atacact			917

<210> 145

<211> 1306

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74)...(694)

<400> 145

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cctggggggtt gcc atg gcc ccc agc cac ctg tca gtg cgg gag atg agg	109
Met Ala Pro Ser His Leu Ser Val Arg Glu Met Arg	
1 5 10	
gaa gat gag aag ccc ctg gtg ctg gag atg ctg aag gcc gcc gtg aag	157
Glu Asp Glu Lys Pro Leu Val Leu Glu Met Leu Lys Ala Gly Val Lys	
15 20 25	

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gac acg gaa aac cgc gtg gcc ctc cat gcc ttg aca cgg ccg ccg gcc	205
Asp Thr Glu Asn Arg Val Ala Leu His Ala Leu Thr Arg Pro Pro Ala	
30 35 40	
ctg ctc ctc ctg gcg gcg gcc agc agc ggc ctg cgc ttt gtc ctg gct	253
Leu Leu Leu Leu Ala Ala Ala Ser Ser Gly Leu Arg Phe Val Leu Ala	
45 50 55 60	
tcc ttc gcc ctg gcc ctc ctc ctg ccg gtg ttc ctg gct gtg gcc gcc	301
Ser Phe Ala Leu Ala Leu Leu Leu Pro Val Phe Leu Ala Val Ala Ala	
65 70 75	
gtg aag ctg ggc ctg cgg gcc cga tgg ggc tcg ctg cct ccg ccg ggt	349
Val Lys Leu Gly Leu Arg Ala Arg Trp Gly Ser Leu Pro Pro Pro Gly	
80 85 90	
ggc ctg ggg gcc ccc tgg gtg gcc gtg cgg ggc tcc ggt gac gtg tgt	397
Gly Leu Gly Gly Pro Trp Val Ala Val Arg Gly Ser Gly Asp Val Cys	
95 100 105	
ggg gtc ctg gct ctg gcc cct ggc aca aat gca ggg gac ggg gcc cgg	445
Gly Val Leu Ala Leu Ala Pro Gly Thr Asn Ala Gly Asp Gly Ala Arg	
110 115 120	
gtc acc cgc ctg tot gtc tot cgc tgg cac cgc cgc cgg ggc gtg gcc	493
Val Thr Arg Leu Ser Val Ser Arg Trp His Arg Arg Arg Gly Val Gly	
125 130 135 140	
agg agg ctg ctg gcc ttc gcg gag gcc cgg gct cgg gcc tgg gct ggg	541
Arg Arg Leu Leu Ala Phe Ala Glu Ala Arg Ala Arg Ala Trp Ala Gly	
145 150 155	
ggc atg ggg gag ccc cgg gcc cgg ctc gtg gtc ccc gtg gct gtg gcc	589
Gly Met Gly Glu Pro Arg Ala Arg Leu Val Val Pro Val Ala Val Ala	
160 165 170	
gcc tgg ggg gtg gga ggg atg ctg gag ggc tgt gcc tac cag gcc gag	637
Ala Trp Gly Val Gly Gly Met Leu Glu Gly Cys Gly Tyr Gln Ala Glu	
175 180 185	
ggg ggc tgg gcc tgc ctg gcc tac acg ctg gtg agg gaa ttc agc aaa	685
Gly Gly Trp Gly Cys Leu Gly Tyr Thr Leu Val Arg Glu Phe Ser Lys	
190 195 200	
gac ctg tgaagctaca gactgacagc cagggcaggg gaggagggag gggcgccag	740
Asp Leu	

221/233

205

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cacctgatga tcgcctactg totgcggtt cttttacctg ctctccctca gtgagtcctc      800
aaccaccctg ggcccagaaa cagaggcctg ccgaggggag gagcctggcc tctgtccacc      860
cgtcagcagt gtgaagtctg ttgtgtttga gcttctcaga gtggaatgac tccttttctc      920
tcttgccctt cgggggcttc tcgaggtcag cctctccaac ccctacctca gctcctgtct      980
gcactgagaa acctccccgg gtgatgtctg caaagtctgt gctgtccgtg ccccaggctg     1040
ggagagctat ctggggaggg ggagaggagg ccgagcagaa tacaccccag agttagggtt     1100
tgcgactccg cctccctggg acctggattg ggtcagatgc ctgtccttgg aggggacaag     1160
gttgactgct taggaggcgc gacgcacagg gctgccaggc ctggccctc tctgggaagg     1220
ttgagagctg agacgggcag ccctgtccct tctccagat ccgtctggtt ttttacccg      1280
tttgtaata aagcctgaaa ccgctt                                           1306

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<210> 146

<211> 2022

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (118)...(1416)

<400> 146

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gcgcgcccg gggactcgca ttccccggtt cccctccac cccacgcggc ctggacc      117
atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc      165
Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
      1              5              10              15
cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc      213
Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
      20              25              30
cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc      261
Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
      35              40              45
ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac      309
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
      50              55              60
tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt      357

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Tyr	Leu	Glu	Thr	Gly	Arg	Gly	Leu	Cys	Phe	Pro	Leu	Val	Lys	Ala	Cys	
65					70					75					80	
gtg	ttt	ggc	aat	gag	ccc	aag	gcc	tct	gat	gag	gtt	ccc	ctg	gcg	ccc	405
Val	Phe	Gly	Asn	Glu	Pro	Lys	Ala	Ser	Asp	Glu	Val	Pro	Leu	Ala	Pro	
				85					90					95		
cga	aca	gag	gcg	gca	gag	acc	acc	ccg	atg	tgg	cag	gcc	ctg	aag	ctg	453
Arg	Thr	Glu	Ala	Ala	Glu	Thr	Thr	Pro	Met	Trp	Gln	Ala	Leu	Lys	Leu	
				100				105					110			
ctc	ttc	tgt	gcc	aca	ggg	ctc	cag	gtg	tct	tat	ctg	act	tgg	ggg	gtg	501
Leu	Phe	Cys	Ala	Thr	Gly	Leu	Gln	Val	Ser	Tyr	Leu	Thr	Trp	Gly	Val	
			115				120						125			
ctg	cag	gaa	aga	gtg	atg	acc	cgc	agc	tat	ggg	gcc	aca	gcc	aca	tca	549
Leu	Gln	Glu	Arg	Val	Met	Thr	Arg	Ser	Tyr	Gly	Ala	Thr	Ala	Thr	Ser	
			130				135						140			
ccg	ggg	gag	cgc	ttt	acg	gac	tcg	cag	ttc	ctg	gtg	cta	atg	aac	cga	597
Pro	Gly	Glu	Arg	Phe	Thr	Asp	Ser	Gln	Phe	Leu	Val	Leu	Met	Asn	Arg	
145				150					155					160		
gtg	ctg	gca	ctg	att	gtg	gct	ggc	ctc	tcc	tgt	gtt	ctc	tgc	aag	cag	645
Val	Leu	Ala	Leu	Ile	Val	Ala	Gly	Leu	Ser	Cys	Val	Leu	Cys	Lys	Gln	
				165					170					175		
ccc	cgg	cat	ggg	gca	ccc	atg	tac	cgg	tac	tcc	ttt	gcc	agc	ctg	tcc	693
Pro	Arg	His	Gly	Ala	Pro	Met	Tyr	Arg	Tyr	Ser	Phe	Ala	Ser	Leu	Ser	
			180					185					190			
aat	gtg	ctt	agc	agc	tgg	tgc	caa	tac	gaa	gct	ctt	aag	ttc	gtc	agc	741
Asn	Val	Leu	Ser	Ser	Trp	Cys	Gln	Tyr	Glu	Ala	Leu	Lys	Phe	Val	Ser	
			195				200						205			
ttc	ccc	acc	cag	gtg	ctg	gcc	aag	gcc	tct	aag	gtg	atc	cct	gtc	atg	789
Phe	Pro	Thr	Gln	Val	Leu	Ala	Lys	Ala	Ser	Lys	Val	Ile	Pro	Val	Met	
			210				215						220			
ctg	atg	gga	aag	ctt	gtg	tct	cgg	cgc	agc	tac	gaa	cac	tgg	gag	tac	837
Leu	Met	Gly	Lys	Leu	Val	Ser	Arg	Arg	Ser	Tyr	Glu	His	Trp	Glu	Tyr	
225				230					235					240		
ctg	aca	gcc	aca	ctc	atc	tcc	att	ggg	gtc	agc	atg	ttt	ctg	cta	tcc	885
Leu	Thr	Ala	Thr	Leu	Ile	Ser	Ile	Gly	Val	Ser	Met	Phe	Leu	Leu	Ser	
				245					250					255		

223/233

agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc	933
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu	
260 265 270	
atc tta ctg gca ggt tat att gct ttt gac agc ttc acc tca aac tgg	981
Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp	
275 280 285	
cag gat gcc ctg ttt gcc tat aag atg tca tcg gtg cag atg atg ttt	1029
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe	
290 295 300	
ggg gtc aat ttc ttc tcc tgc ctc ttc aca gtg ggc tca ctg cta gaa	1077
Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu	
305 310 315 320	
cag ggg gcc cta ctg gag gga acc cgc ttc atg ggg cga cac agt gag	1125
Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu	
325 330 335	
ttt gct gcc cat gcc ctg cta ctc tcc atc tgc tcc gca tgt ggc cag	1173
Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln	
340 345 350	
ctc ttc atc ttt tac acc att ggg cag ttt ggg gct gcc gtc ttc acc	1221
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr	
355 360 365	
atc atc atg acc ctc cgc cag gcc ttt gcc atc ctt ctt tcc tgc ctt	1269
Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu	
370 375 380	
ctc tat ggc cac act gtc act gtg gtg gga ggg ctg ggg gtg gct gtg	1317
Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val	
385 390 395 400	
gtc ttt gct gcc ctc ctg ctc aga gtc tac gcg cgg ggc cgt cta aag	1365
Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys	
405 410 415	
caa cgg gga aag aag gct gtg cct gtt gag tct cct gtg cag aag gtt	1413
Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val	
420 425 430	
tgaggggt ggaaagggcc tgaggggtga agtgaatat gaccctccca ccatccctt	1470
ctgctgtaac ctctgagggga gctggctgaa agggcaaat gcaggtgttt tctcagtac	1530

224/233

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acagaccagc tctgcagcag gggattgggg agcccaggag gcagccttcc cttttgcctt 1590
aagtcaccca tcttccagta agcagtttat tctgagcccc gggggttagac agtcctcagt 1650
gagggggtttt ggggagtttg gggccaagag agcataggta ggttccacag ttactcttcc 1710
cacaagtccc ctttaagtctt gccctagctg tgctctgcca ccttccagac tcactccctt 1770
ctgcaaatac ctgcatttct taccctgggtg agaaaagcac aagcgggtgta ggctccaatg 1830
ctgctttccc aggaggggtga agatgggtgct gtgctgagga aaggggatgc agagccctgc 1890
ccagcaccac cacctcctat gctcctggat ccttaggctc tgttccatga gcctgttgca 1950
gggttttgta ctttagaaat gtaacttttt gctcttataa ttttatttta ttaaattaaa 2010
ttactgcagt gg 2022

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<210> 147

<211> 1227

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (75)...(995)

<400> 147

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gaactgtaggg ggcc atg ggg cac cgg acc ctg gtc ctg ccc tgg gtg ctg 110
      Met Gly His Arg Thr Leu Val Leu Pro Trp Val Leu
              1              5              10
ctg acc ttg tgt gtc act gcg ggg acc ccg gag gtg tgg gtt caa gtt 158
Leu Thr Leu Cys Val Thr Ala Gly Thr Pro Glu Val Trp Val Gln Val
      15              20              25
cgg atg gag gcc acc gag ctc tcg tcc ttc acc atc cgt tgt ggg ttc 206
Arg Met Glu Ala Thr Glu Leu Ser Ser Phe Thr Ile Arg Cys Gly Phe
      30              35              40
ctg ggg tct ggc tcc atc tcc ctg gtg act gtg agc tgg ggg ggc ccc 254
Leu Gly Ser Gly Ser Ile Ser Leu Val Thr Val Ser Trp Gly Gly Pro
      45              50              55              60
gac ggt gct ggg ggg acc acg ctg gct gtg ttg cac cca gaa cgt ggc 302
Asp Gly Ala Gly Gly Thr Thr Leu Ala Val Leu His Pro Glu Arg Gly
      65              70              75
atc cgg caa tgg gcc cct gct cgc cag gcc cgc tgg gaa acc cag agc 350

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225/233

Ile Arg Gln Trp Ala Pro Ala Arg Gln Ala Arg Trp Glu Thr Gln Ser	
80 85 90	
agc atc tct ctc atc ctg gaa ggc tct ggg gcc agc agc ccc tgc gcc	398
Ser Ile Ser Leu Ile Leu Glu Gly Ser Gly Ala Ser Ser Pro Cys Ala	
95 100 105	
aac acc acc ttc tgc tgc aag ttt gcg tcc ttc cct gag ggc tcc tgg	446
Asn Thr Thr Phe Cys Cys Lys Phe Ala Ser Phe Pro Glu Gly Ser Trp	
110 115 120	
gag gcc tgt ggg agc ctc ccg ccc agc tca gac cca ggg ctc tct gcc	494
Glu Ala Cys Gly Ser Leu Pro Pro Ser Ser Asp Pro Gly Leu Ser Ala	
125 130 135 140	
ccg ccg act cct gcc ccc att ctg cgg gca gac ctg gcc ggg atc ttg	542
Pro Pro Thr Pro Ala Pro Ile Leu Arg Ala Asp Leu Ala Gly Ile Leu	
145 150 155	
ggg gtc tca gga gtc ctc ctc ttt ggc tgt gtc tac ctc ctt cat ctg	590
Gly Val Ser Gly Val Leu Leu Phe Gly Cys Val Tyr Leu Leu His Leu	
160 165 170	
ctg cgc cga cat aag cac cgc cct gcc cct agg ctc cag ccg tcc cgc	638
Leu Arg Arg His Lys His Arg Pro Ala Pro Arg Leu Gln Pro Ser Arg	
175 180 185	
acc agc ccc cag gca ccg aga gca cga gca tgg gca cca agc cag gcc	686
Thr Ser Pro Gln Ala Pro Arg Ala Arg Ala Trp Ala Pro Ser Gln Ala	
190 195 200	
tcc cag gct gct ctt cac gtc cct tat gcc act atc aac acc agc tgc	734
Ser Gln Ala Ala Leu His Val Pro Tyr Ala Thr Ile Asn Thr Ser Cys	
205 210 215 220	
cgc cca gct act ttg gac aca gct cac ccc cat ggg ggg ccg tcc tgg	782
Arg Pro Ala Thr Leu Asp Thr Ala His Pro His Gly Gly Pro Ser Trp	
225 230 235	
tgg gcg tca ctc ccc acc cac gct gca cac cgg ccc cag ggc cct gcc	830
Trp Ala Ser Leu Pro Thr His Ala Ala His Arg Pro Gln Gly Pro Ala	
240 245 250	
gcc tgg gcc tcc aca ccc atc cct gca cgt ggc agc ttt gtc tct gtt	878
Ala Trp Ala Ser Thr Pro Ile Pro Ala Arg Gly Ser Phe Val Ser Val	
255 260 265	

226/233

gag aat gga ctc tac gct cag gca ggg gag agg cct cct cac act ggt 926
 Glu Asn Gly Leu Tyr Ala Gln Ala Gly Glu Arg Pro Pro His Thr Gly
 270 275 280
 ccc ggc ctc act ctt ttc cct gac cct cgg ggg ccc agg gcc atg gaa 974
 Pro Gly Leu Thr Leu Phe Pro Asp Pro Arg Gly Pro Arg Ala Met Glu
 285 290 295 300
 gga ccc tta gga gtt cga tgagagagac catgaggcca ctgggctt 1020
 Gly Pro Leu Gly Val Arg
 305
 tccccctccc aggcctcctg ggtgtcaccc ccttacttta attottgggc ctccaataag 1080
 tgccccatag gtgtctggcc agggccacct gctgcggatg tggctgtgtg gctgtgtgtg 1140
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 agtcagcaac acagtttctc tgatgtc 1227

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 ggcgagacc ggagcgccgc tcgcccaga cttacttccc cggctcagca gggaaagggt 180
 cctagaaggt gacgcggac ggt atg caa agt tgt gaa tcc agt ggt gac agt 233
 Met Gln Ser Cys Glu Ser Ser Gly Asp Ser
 1 5 10
 gcg gat gac cct ctc agt cgc ggc cta cgg aga agg gga cag cct cgt 281
 Ala Asp Asp Pro Leu Ser Arg Gly Leu Arg Arg Arg Gly Gln Pro Arg
 15 20 25
 gtg gtg gtg atc ggc gcc ggc ttg gct ggc ctg gct gca gcc aaa gca 329
 Val Val Val Ile Gly Ala Gly Leu Ala Gly Leu Ala Ala Ala Lys Ala
 30 35 40
 ctt ctt gag cag ggt ttc acg gat gtc act gtg ctt gag gct tcc agc 377

227/233

Leu Leu Glu Gln Gly Phe Thr Asp Val Thr Val Leu Glu Ala Ser Ser	
45 50 55	
cac atc gga ggc cgt gtg cag agt gtg aaa ctt gga cac gcc acc ttt	425
His Ile Gly Gly Arg Val Gln Ser Val Lys Leu Gly His Ala Thr Phe	
60 65 70	
gag ctg gga gcc acc tgg atc cat ggc tcc cat ggg aac cct atc tat	473
Glu Leu Gly Ala Thr Trp Ile His Gly Ser His Gly Asn Pro Ile Tyr	
75 80 85 90	
cat cta gca gaa gcc aac ggc ctc ctg gaa gag aca acc gat ggg gaa	521
His Leu Ala Glu Ala Asn Gly Leu Leu Glu Glu Thr Thr Asp Gly Glu	
95 100 105	
cgc agc gtg ggc cgc atc agc ctc tat tcc aag aat ggc gtg gcc tgc	569
Arg Ser Val Gly Arg Ile Ser Leu Tyr Ser Lys Asn Gly Val Ala Cys	
110 115 120	
tac ctt acc aac cac ggc cgc agg atc ccc aag gac gtg gtt gag gaa	617
Tyr Leu Thr Asn His Gly Arg Arg Ile Pro Lys Asp Val Val Glu Glu	
125 130 135	
ttc agc gat tta tac aac gag gtc tat aac ttg acc cag gag ttc ttc	665
Phe Ser Asp Leu Tyr Asn Glu Val Tyr Asn Leu Thr Gln Glu Phe Phe	
140 145 150	
cgg cac gat aaa cca gtc aat gct gaa agt caa aat agc gtg ggg gtg	713
Arg His Asp Lys Pro Val Asn Ala Glu Ser Gln Asn Ser Val Gly Val	
155 160 165 170	
ttc acc cga gag gag gtg cgt aac cgc atc agg aat gac cct gac gac	761
Phe Thr Arg Glu Glu Val Arg Asn Arg Ile Arg Asn Asp Pro Asp Asp	
175 180 185	
cca gag gct acc aag cgc ctg aag ctc gcc atg atc cag cag tac ctg	809
Pro Glu Ala Thr Lys Arg Leu Lys Leu Ala Met Ile Gln Gln Tyr Leu	
190 195 200	
aag gtg gag agc tgt gag agc agc tca cac agc atg gac gag gtg tcc	857
Lys Val Glu Ser Cys Glu Ser Ser Ser His Ser Met Asp Glu Val Ser	
205 210 215	
ctg agc gcc ttc ggg gag tgg acc gag atc ccc ggc gct cac cac atc	905
Leu Ser Ala Phe Gly Glu Trp Thr Glu Ile Pro Gly Ala His His Ile	
220 225 230	

228/233

atc ccc tcg ggc ttc atg cgg gtt gtg gag ctg ctg gcg gag ggc atc	953
Ile Pro Ser Gly Phe Met Arg Val Val Glu Leu Leu Ala Glu Gly Ile	
235 240 245 250	
cct gcc cac gtc atc cag cta ggg aaa cct gtc cgc tgc att cac tgg	1001
Pro Ala His Val Ile Gln Leu Gly Lys Pro Val Arg Cys Ile His Trp	
255 260 265	
gac cag gcc tca gcc cgc ccc aga ggc cct gag att gag ccc cgg ggt	1049
Asp Gln Ala Ser Ala Arg Pro Arg Gly Pro Glu Ile Glu Pro Arg Gly	
270 275 280	
gag ggc gac cac aat cac gac act ggg gag ggt ggc cag ggt gga gag	1097
Glu Gly Asp His Asn His Asp Thr Gly Glu Gly Gly Gln Gly Gly Glu	
285 290 295	
gag ccc cgg ggg ggc agg tgg gat gag gat gag cag tgg tcg gtg gtg	1145
Glu Pro Arg Gly Gly Arg Trp Asp Glu Asp Glu Gln Trp Ser Val Val	
300 305 310	
gtg gag tgc gag gac tgt gag ctg atc ccg gcg gac cat gtg att gtg	1193
Val Glu Cys Glu Asp Cys Glu Leu Ile Pro Ala Asp His Val Ile Val	
315 320 325 330	
acc gtg tcg cta ggt gtg cta aag agg cag tac acc agt ttc ttc cgg	1241
Thr Val Ser Leu Gly Val Leu Lys Arg Gln Tyr Thr Ser Phe Phe Arg	
335 340 345	
cca ggc ctg ccc aca gag aag gtg gct gcc atc cac cgc ctg ggc att	1289
Pro Gly Leu Pro Thr Glu Lys Val Ala Ala Ile His Arg Leu Gly Ile	
350 355 360	
ggc acc acc gac aag atc ttt ctg gaa ttc gag gag ccc ttc tgg ggc	1337
Gly Thr Thr Asp Lys Ile Phe Leu Glu Phe Glu Glu Pro Phe Trp Gly	
365 370 375	
cct gag tgc aac agc cta cag ttt gtg tgg gag gac gaa gcg gag agc	1385
Pro Glu Cys Asn Ser Leu Gln Phe Val Trp Glu Asp Glu Ala Glu Ser	
380 385 390	
cac acc ctc acc tac cca cct gag ctc tgg tac cgc aag atc tgc ggc	1433
His Thr Leu Thr Tyr Pro Pro Glu Leu Trp Tyr Arg Lys Ile Cys Gly	
395 400 405 410	
ttt gat gtc ctc tac ccg cct gag cgc tac ggc cat gtg ctg agc ggc	1481
Phe Asp Val Leu Tyr Pro Pro Glu Arg Tyr Gly His Val Leu Ser Gly	

229/233

415	420	425	
tgg atc tgc ggg gag gag gcc ctc gtc atg gag aag tgt gat gac gag			1529
Trp Ile Cys Gly Glu Glu Ala Leu Val Met Glu Lys Cys Asp Asp Glu			
430	435	440	
gca gtg gcc gag atc tgc acg gag atg ctg cgt cag ttc aca ggg aac			1577
Ala Val Ala Glu Ile Cys Thr Glu Met Leu Arg Gln Phe Thr Gly Asn			
445	450	455	
ccc aac att cca aaa cct cgg cga atc ttg cgc tcg gcc tgg ggc agc			1625
Pro Asn Ile Pro Lys Pro Arg Arg Ile Leu Arg Ser Ala Trp Gly Ser			
460	465	470	
aac cct tac ttc cgc ggc tcc tat tca tac acg cag gtg ggc tcc agc			1673
Asn Pro Tyr Phe Arg Gly Ser Tyr Ser Tyr Thr Gln Val Gly Ser Ser			
475	480	485	490
ggg gcg gat gtg gag aag ctg gcc aag ccc ctg ccg tac acg gag agc			1721
Gly Ala Asp Val Glu Lys Leu Ala Lys Pro Leu Pro Tyr Thr Glu Ser			
495	500	505	
tca aag aca gcg ccc atg cag gtg ctg ttt tcc ggt gag gcc acc cac			1769
Ser Lys Thr Ala Pro Met Gln Val Leu Phe Ser Gly Glu Ala Thr His			
510	515	520	
cgc aag tac tat tcc acc acc cac ggt gct ctg ctg tcc ggc cag cgt			1817
Arg Lys Tyr Tyr Ser Thr Thr His Gly Ala Leu Leu Ser Gly Gln Arg			
525	530	535	
gag gct gcc cgc ctc att gag atg tac cga gac ctc ttc cag cag ggg			1865
Glu Ala Ala Arg Leu Ile Glu Met Tyr Arg Asp Leu Phe Gln Gln Gly			
540	545	550	
acc tgagggtgt cctcgtgtgt gagaagagcc actaactcgt gacctccagc ct			1920
Thr			
555			
gccccttgct gcggtgtgt cctgccttcc tgatcctctg tagaaaggat ttttatcttc			1980
tgtagagcta gccgccctga ctgccttcag acctggccct gtagcttttc tttttctcca			2040
ggctgggccc tgagcaggtg ggccgttgag ttacctctgt gctggatccc gtgccccac			2100
ttgcctaccc totgtcctgc cttgttattg taagtgcctt caatactttg cattttggga			2160
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<210> 149

230/233

<211> 1493

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (93)...(845)

<400> 149

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Met Gly Ser Gln His Ser Ala	
1 5	
gct gct cgc ccc tcc tcc tgc agg cga aag caa gaa gat gac agg gac	161
Ala Ala Arg Pro Ser Ser Cys Arg Arg Lys Gln Glu Asp Asp Arg Asp	
10 15 20	
ggg ttg ctg gct gaa cga gag cag gaa gaa gcc att gct cag ttc cca	209
Gly Leu Leu Ala Glu Arg Glu Gln Glu Glu Ala Ile Ala Gln Phe Pro	
25 30 35	
tat gtg gaa ttc acc ggg aga gat agc atc acc tgt ctc acg tgc cag	257
Tyr Val Glu Phe Thr Gly Arg Asp Ser Ile Thr Cys Leu Thr Cys Gln	
40 45 50 55	
ggg aca ggc tac att cca aca gag caa gta aat gag ttg gtg gct ttg	305
Gly Thr Gly Tyr Ile Pro Thr Glu Gln Val Asn Glu Leu Val Ala Leu	
60 65 70	
atc cca cac agt gat cag aga ttg cgc cct cag cga act aag caa tat	353
Ile Pro His Ser Asp Gln Arg Leu Arg Pro Gln Arg Thr Lys Gln Tyr	
75 80 85	
gtc ctc ctg tcc atc ctg ctt tgt ctc ctg gca tct ggt ttg gtg gtt	401
Val Leu Leu Ser Ile Leu Leu Cys Leu Leu Ala Ser Gly Leu Val Val	
90 95 100	
ttc ttc ctg ttt ccg cat tca gtc ctt gtg gat gat gac ggc atc aaa	449
Phe Phe Leu Phe Pro His Ser Val Leu Val Asp Asp Asp Gly Ile Lys	
105 110 115	
gtg gtg aaa gtc aca ttt aat aag caa gac tcc ctt gta att ctc acc	497
Val Val Lys Val Thr Phe Asn Lys Gln Asp Ser Leu Val Ile Leu Thr	
120 125 130 135	

231/233

atc atg gcc acc ctg aaa atc agg aac tcc aac ttc tac acg gtg gca	545
Ile Met Ala Thr Leu Lys Ile Arg Asn Ser Asn Phe Tyr Thr Val Ala	
140 145 150	
gtg acc agc ctg tcc agc cag att cag tac atg aac aca gtg gtc agt	593
Val Thr Ser Leu Ser Ser Gln Ile Gln Tyr Met Asn Thr Val Val Ser	
155 160 165	
aca tat gtg act act aac gtc tcc ctt att cca cct cgg agt gag caa	641
Thr Tyr Val Thr Thr Asn Val Ser Leu Ile Pro Pro Arg Ser Glu Gln	
170 175 180	
ctg gtg aat ttt acc ggg aag gcc gag atg gga gga ccg ttt tcc tat	689
Leu Val Asn Phe Thr Gly Lys Ala Glu Met Gly Gly Pro Phe Ser Tyr	
185 190 195	
gtg tac ttc ttc tgc acg gta cct gag atc ctg gtg cac aac ata gtg	737
Val Tyr Phe Phe Cys Thr Val Pro Glu Ile Leu Val His Asn Ile Val	
200 205 210 215	
atc ttc atg cga act tca gtg aag att tca tac att ggc ctc atg acc	785
Ile Phe Met Arg Thr Ser Val Lys Ile Ser Tyr Ile Gly Leu Met Thr	
220 225 230	
cag agc tcc ttg gag aca cat cac tat gtg gat tgt gga gga aat tcc	833
Gln Ser Ser Leu Glu Thr His His Tyr Val Asp Cys Gly Gly Asn Ser	
235 240 245	
aca got att taacaactgc tattggttct tccacacagc gcctgtagaa gagagcac	890
Thr Ala Ile	
250	
agcatatgtt cccaaggcct gagttotgga cctaccccca cgtggtgtaa gcagaggagg	950
aattggttca cttaactccc agcaaacatc ctctgccac ttaggaggaa acacctccct	1010
atggtaccat ttatgtttct cagaaccagc agaatcagtg cctagcctgt gccagcaaa	1070
tagttggcac tcaataaaga tttgcagaat ttaatacaga tcttttcagc tgttottagg	1130
gcattataaa tggaaatcat aacgtggttc taggttatca aaccatggag tgatgtggag	1190
ctaggattgt gagtgacctg caggccatta tcagtgcctc atctgtgcag aagtcgcagc	1250
agagagggac catccaaata cctaagagaa aacagacctc gtcaggatat gaatttgttt	1310
cagctgttcc caaaggcctg ggagotTTTT gaaaagaaag aaaaaagtgt gttggctttt	1370
TTTTTTTTta gaaagttaga attgttttta ccaagagtct atgtggggct tgattcaccc	1430
tccatccatt ggctggaaca tggattgggg atttgataga aaaataaacc ctgcttttga	1490
ttc	1493

232/233

<210> 150

<211> 1264

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26)...(550)

<400> 150

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                               1           5

aaa cag ggg gtc tca gcc aag aat caa ggt gcc cat gac cca gac tat      100
Lys Gln Gly Val Ser Ala Lys Asn Gln Gly Ala His Asp Pro Asp Tyr
   10           15           20           25

gag aat atc acc ttg gcc ttc aaa aat cag gac cat gca aag ggt ggt      148
Glu Asn Ile Thr Leu Ala Phe Lys Asn Gln Asp His Ala Lys Gly Gly
           30           35           40

cat tca cga ccc acg agc caa gtc cca gcc cag tgc agg ccg ccc tca      196
His Ser Arg Pro Thr Ser Gln Val Pro Ala Gln Cys Arg Pro Pro Ser
           45           50           55

gac tcc acc cag gtc ccc tgc tgg ttg tac aga gcc atc ctg agc ctg      244
Asp Ser Thr Gln Val Pro Cys Trp Leu Tyr Arg Ala Ile Leu Ser Leu
           60           65           70

tac atc ctc ctg gcc ctg gcc ttt gtc ctc tgc atc atc ctg tca gcc      292
Tyr Ile Leu Leu Ala Leu Ala Phe Val Leu Cys Ile Ile Leu Ser Ala
           75           80           85

ttc atc atg gtg aag aat gct gag atg tcc aag gag ctg ctg ggc ttt      340
Phe Ile Met Val Lys Asn Ala Glu Met Ser Lys Glu Leu Leu Gly Phe
           90           95           100           105

aaa agg gag ctt tgg aat gtc tca aac tcc gta caa gca tgc gaa gag      388
Lys Arg Glu Leu Trp Asn Val Ser Asn Ser Val Gln Ala Cys Glu Glu
           110           115           120

aga cag aag aga ggc tgg gat tcc gtt cag cag agc atc acc atg gtc      436
Arg Gln Lys Arg Gly Trp Asp Ser Val Gln Gln Ser Ile Thr Met Val

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233/233

125	130	135	
agg agc aag att gat aga tta gag acg aca tta gca ggc ata aaa aac			484
Arg Ser Lys Ile Asp Arg Leu Glu Thr Thr Leu Ala Gly Ile Lys Asn			
140	145	150	
att gac aca aag gta cag aaa atc ttg gag gtg ctg cag aaa atg cca			532
Ile Asp Thr Lys Val Gln Lys Ile Leu Glu Val Leu Gln Lys Met Pro			
155	160	165	
cag tcc tca cct caa taaatgagag gacattgtgg cagccaaagc cac			580
Gln Ser Ser Pro Gln			
170			
aacttggaag atgggggtgc aactgccaac gaagacggga aatgaccccc cccccagcc			640
tagtgtgaac ctgcccctcg tcccacgtat agaaaaacct cgagtcattg tgaatgagt			700
tctcgagatt gctcgtgtgt gtgtacacct gcgtgcgtgt gtgtgcgtgt gtgcgcgtgt			760
gttcgtgtat gtgcgtgtgt gcgtgcgcgt gtgtgtgcat ttgcaaagg gtggacattt			820
cagtgtatct cccagaaagg tgatgaatga ataggactga gagtcacagt gaatgtggca			880
tgcatgcctg tgtcatgtga catatgtgag tctcgccatg tcacgggtggg tggctgtgtc			940
tgagcacctc cagcagatgt cactctgagt gtgggtgttg gtgacatgca ttgcacgggc			1000
ctgtctccct gtttgtgtaa acatactaga gtatactgcg gcgtgttttc tgtctaccca			1060
tgtcatggtg ggggagattt atctccgtac atgtgggtgt cgccatgtgt gccctgtcac			1120
tatctgtggc tgggtgaacg gctgtgtcat tatgagtgtg ccgagttatg ccaccctgtg			1180
tgotcagggc acatgcacac agacatttat ctctgcactc acattttgtg acttatgaag			1240
ataaataaag tcaagggaaa acag			1264